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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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n on:	June	4, 09:27:48 ; Search tim
		(without alignments) 9398.758 Million cell updates/sec
Title: Perfect score: Sequence:	US-1 363 1 at	US-10-024-579-4 363 1 atggtggtagtcacgggggggtagtcctagcaggtgattag 363
Scoring table:	IDENT] Gapop	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272	272 segs, 21671516995 residues
Total number of	hits	satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: length:	h: 0 h: 2000000000
Post-processing:		Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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		gb_ntg:*
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		3b_pl:* ab pr:*
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	26.	em vi:*
	30:	em htg hum:*
	32:	em_htg_other:*
	33:	em htg mus: * em htg nl: *
	35:	em_htg_rod:*
	36:	em htg man: *
	38:	em sy: *
	39:	em htgo hum:
		em_itgo_mus:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Grisl08525.

Homo sapiens (human)

EMARYOFA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1124)

E 2002540791-A 2 Danace_2002;

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E 4 (base 2000 JP 2000609571

E 604-APR-2000 JP 2000609571

E 7 (base 2000 JP 2000609571)

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E 7 (base 2000 JP 2000609571)

E 8 (base 2000 JP 2000609571)

E 9 (base 2000 JP 20
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    .1124
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Novel Thuman ion channel-related proteins and polynucleotides encoding the same
Patent: WO 0206826-A 8 06-SEP-2002;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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100.0%; Pred. No. 3.1e-72;
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100.0%; Score 363; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.3e-72;
Matches 363; Conservative 0; Mismatches 0;
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WO 02068626-A 4 06-SEP-2002;
Genetics Incorporated (US)
Location/Qualifiers
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/db _xref="taxon:9606"
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Seguence 8 from Patent WO02068626.
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700te="K.tetra; Region: K+ channel tetramerisation domain.

70to-E.K.tetrainal, cytoplasmic tetramerisation domain (TI) of

71h N-terminal, cytoplasmic tetramerisation domain (TI) of

72 voltage-gated K+ channels encodes molecular determinants

73 for subfamily-specific assembly of alpha-subunits into

74 functional tetrameric channels. It is distantly related to

74 the BTB/POZ domain pfam00651"

74 Ab_xref="CDD:pfam02214"
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HPGDVLAFLEASGDLPPRERVRAVYERAGYYAGPLEQLEAMOPLKARSKRQAFTGLM
PYROHLERIVEIARIAAVORKAR FAKLKVCYPKERNPITPYECPLLAKSIR FERSESD
GQLPEHHCRVDVSFGPREAVADVYDLLHCLYTDLSAQGITVDHQCIGVCDKHLVNHYX
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A.N., Gibbs, R.A.
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Matches 318; Conservative 0; Mismatches 2; Indels 0;
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/note="UHH UB"
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/db_xref="LocusID:154881"
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/gene="KCTD7"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mansia; Strausberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Alschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,

Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Nocley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

M.D. Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC042482 1211 bp mRNA linear PRI 04-NOV-2003 Homo sapiens potassium channel tetramerisation domain containing 7, mRNA (cDNA clone MGC:34731 IMAGE:5165722), complete cds.
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., LoulBeged, H.,
                                                                                                                                                       240
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                                                                                                                                                                                                                                                              TTCAGIGGGCGCCACTACAICCCCACGGACTCCGAGGGCCGGTACTTCAICGACCGAGAI 300
                                                                                                                                                                                                                                                                                          268 TTCAGTGGGCGGCACTACATCCCCACGACTCCGAGGGCCGGTACTTCATCATCGACCGAGAT 327
                                                                                                  Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                      CACTTCACTACTACCACCTGTCCCACACTACGAAGACACCATGTTGGCAGCCATG
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayeration: Life Technologies, Inc.
CDNA Library Prayeration: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing Conter
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/tissue type="brain"
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/note="cloning vector: pME18SFL3"
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Best Local Similarity 99.4%; Pred. No. 8.3e-62;
Matches 318; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                 1. .2576
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Obhima, A., Takahashi-Pujii, A., Tanase, T., Imose, N., Takeuchi, K.,
Arita, M., Musablino, K., Yuuki, H., Hara, H., Sugiyama, T., Irle, R.,
Otsuki, T., Sato, H., Ota, T., Wakanatsu, A., Ishii, S., Yamamoto, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 GCGCTCCCTGCTGCCACAGAATTTCCTGAGGTTGTTCCCCTTAACATGGGGCCT
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Patent: BP 1293569-A 1045 19-MAR-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
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Sequence 1045 from Patent BP1293569.
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/ Once="unmamed protein product" |
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Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Primates; Catarrhini; Hominidae; Homo

us-10-024-579-4.rge

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Wilson, R
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AUTHORS
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JP 2002345492-A/127
03-D02245492-A/127
03-D02-2002
D 2002049009
OSAMU CHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIKA
C12N15/09, C07K14/47//A61K31/711, A61K38/00, A61K25/00,
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1 (Bases 1 to 4807)

Chara,O., Nagase,T. and Nakajima,D.

Novel genes and proteins encoded by the genes

Patent: JP 2002345492-A 127 03-DEC-2002;
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AGIP22/14,
AGIP25/18,AGIP35/00,C12N15/00,AGIK37/02
Novel genes and proteins encoded by the genes FH
Location/Qualifiers
CDS
(80). (989).
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                           linear
                    DUB 1414 4807 bp DNA ling Novel genes and proteins encoded by the genes. BD183414
                                                                                                                                                                                                                                                                                                                                     (686) . . (09)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                               BD183414.1 GI:31875614
JP 2002345492-A/127.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 99.1%;
Matches 317; Conservative
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Erro. D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DRIX/GTR7, send mailto:egreen@mhgri.nih.gov, or see http://genome.wustl.edu
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Submitted (02-0CT-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 8, 1999 this sequence version replaced gi:3907522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-NOV-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 135044) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-APR-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, 7 (bases 1 to 135044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (07-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MD 63108, USA
5 (bases 1 to 135044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Mashington University Genome Sequencing Center Center code: WIGSC Web site: http://genome.wustl.edu Context: sapiensSwatson.wustl.edu Context: sapiensSwatson.wustl.edu Center project name: H_DN0756H11
                                                                                                                                                                                                                                        2 (Dases 1 to 135044)
Lamar, B., Le, T. and Wohldmann, P.
The sequence of Homo sapiens PAC clone RP4-756H11
Unpublished (2001)
3 (Dases 1 to 135044)
Waterston, R. H.
Mammalia; Butheria; Primates; C
1 (bases 1 to 135044)
Sulston,J.B. and Wilson,R.
Toward a complete human genome
Genome Res. B (11), 1097-1108 (
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Submitted (30-SEP-2000) D
University, 4444 Forest P
6 [bases 1 to 135044)
Waterston, R.
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SOURCE INFORMATION: This clone wes derived from human PAC library RPC1-4, prepared by

PRI 02-OCT-2003

Homo sapiens Homo sapiens Eukaryota; Mețazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

AC006001 Homo sapiens PAC clone RP4-756H11 from 7, complete sequence. AC006001. AC06001.2 GI:5708496

us-10-024-579-4.rge

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Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc.
(http://www.genomesystems.com) or Research Genetics, Inc.
(http://www.respen.com); or from Pieter de Jong.
                                                                                                                 NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP4-756Hll actual end is at base position 135044 of RP4-756Hll.
Location/Qualifiers
1. 135044
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14461. .14592
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8972. 9965 |
8972. 9065 |
9079. 9126 |
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9187. 9229 |
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GenCore	(c) 1993
	Copyright

OM nucleic - nucleic search, using sw model

8, 2004, 07:09:53 ; Search time 357 Seconds (without alignments) (without alignments) (319:596 Million cell updates/sec June Run on:

US-10-024-579-4 363 1 atggtggtagtcacggggcg......tagtcctagcaggtgattag 363 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
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Listing first 45 summaries

genesegn1980s:*
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SUMP		ID		ABS55072	AAH99183	ABX71180	AAA95776	ADA5347	AA111478	ABA53148	AAI32753	ABA4272	ABA22919	AAK26849	AAK01395	ABS26442	AA101392	ABS01448	ABS5507	AAC03296	AAI20691	ABA65740	AA145906	ABA47847	ABA32824	AAK39882
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	40	Query		100.0	87.3	87.3	87.3	87.3	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	60.7	56.1	47.4	47.4	47.4	47.4	47.4	47.4
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ALI GNMENTS

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Human, 88; gene; membrane protein; signal transduction; ion channel; cancer; arthritis; antiviral; cytostatic; antiarthritic; nutritional; cosmetic; SNP; single nucleotide polymorphism.
                                                                                                                                                                                   /product "Membrane protein"
/note= "This CDS is specifically claimed in claim 2"
/*replace(231,A)
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                                                                              Human novel membrane protein cDNA #2.
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                                                                                                                                                               Location/Qualifiers
                 ABS55072 standard; cDNA; 680 BP.
                                                                                                                                                                                                                                                                                                                                                            18-DEC-2001; 2001US-00024579.
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                                                          (first entry)
                                                                                                                                                                          198. .560
                                                                                                                                                                                                                                                                                                                                                                                                (FRID/) FRIDDLE C J. (GERH/) GERHARDT B. (HILB/) HILBUN E. (TURN/) TURNER C A.
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                                                                                                                                            Homo sapiens
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                                                           10-DEC-2002
                                                                                                                                                                                                                                                                                                                                       29-AUG-2002
                                                                                                                                                                                                                 variation
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                                        ABS55072;
                                                                                                                                                                                                                                                                            variation
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RESULT 1
ABS55072
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The invention relates to an isolated mucleic acid molecule encoding a novel human membrane protein/ion channel-related protein, including a covertor sequence encoding the proteins. The nucleic acid and its encoded amino acid sequences are useful in therapeutic, diagnostic and planmacogenomic applications. The nucleic acid sequences and the encoding amino acid sequences are useful in microarrays or other assay formats, to screen a collection of genetic material from patients that have particular medical conditions, and to identify mutations associated with a particular disease, and also in diagnostic or prognostic assays.

Nucleic acid sequences are useful in sometic or prognostic assays.

Nucleic acid sequences and the amino acid sequences are useful in screening of drugs effective in the treatment of symptomatic or phenotypic manifestation perturbing the normal function of a new human screening of drugs effective in the mucleic acid and the amino acid sequences are useful in diagnosis, drug screening, clinical trial monitoring, the treatment of diseases and disorders and in cosmetic or nutritional complications. MHPs are useful to treat a disease, or to therapeutically augment the efficacy of chemotherapeutic agents useful in the treatment of cancer, arthritis or as antiviral agents. The present sequence is a contact and now and acid and contact and c
                                                                                                                  New human ion channel-related nucleic acid sequences useful for the treatment of cancer, arthritis or as antiviral agents, in therapeutic, diagnostic and pharmacogenomic applications.
                                                                                                                                                                                                                                                                                          Disclosure; Page 13; 20pp; English
WPI; 2002-731353/79.
P-PSDB; ABG70921.
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Sequence 680 BP; 126 A; 212 C; 201 G; 139 T; 0 U; 2 Other;

ö 180 240 TCTGACGCCGAAGACGACTTTCTGGAGCCGGCCACGCGACGGCCACGCAGGCGGCGCAC 317 377 CACTICACIACAGGCCTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATG 437 TICAGIGGGGGGCACIACAICCCCACGGACICCGAGGGCCGGIACIICAICGACCGAGAI 300 301 GGCACACACTTTGGGTATGTCTCCCTCTACAATCAACTTTGTAGTCCTAGCAGGTCAT 360 557 198 ATGGTGGTRGTCACGGGGGGGGGGAGCCAAACACCCGTCAGGACGGTGCCATGTCCAGC 257 09 318 GCGCTGCCCCTGCCACAGAGTTTCCTGAGGTTGTTCCCTTAACATCGAGGGGCT 1 ATGGTGGTAGTCACGGGGGGGGGAGCCAGACAGCCGTCGTCAGGACGGTGCCATGTCCAGC GCGCTGCCCTGCCACACAGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGGCT CACTTCACTACACCCTGTCCACACACTGCTACGAAGACACCATGTTGGCAGCCATG 0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-89;
Matches 363; Conservative 0; Mismatches 0; Indels (361 TAG 363 121 378 61 258 181 241 43B 셤 ઠે 셤 8 임 ò 유 ŝ g 8 8 ઠે

Human protein encoding cDNA sequence SEQ ID NO:18 AAH99183 standard; cDNA; 519 BP. 16-OCT-2001 (first entry) AAH99183; AAH99183
110 AAH9
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AC AAH9
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XX XX RESULT 2

antiliflammatory; antitheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide; antibacterial; endocrine; cardiant; central nervous system, virucide; antiagegeque; antimuteary antiulcer; osteopathic; anemata dermatological; antiallergic; antiasthmatic; antidiabethic; corcentic; neuroprotective; antidepressant; nootropic; antidiabetlo; cytostatic; neuropathylactic; rheumatold arthritis; septic shock; pancrealtis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombootroperoperoperopic; allergic chinitis; diabetes; multiple solerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; cancer; ulcer; HIV infection; human immunodeficiency virus; neurological

Homo sapiens.

WO200153455-A2

26-JUL-2001

22-DEC-2000; 2000WO-US035017

23-DEC-1999; 99US-00471275. 21-JAN-2000; 2000US-00488725. 25-APR-2000; 2006US-00552317.

(HYSE-) HYSEQ INC.

rang YT, Liu C, Drmanac RT;

2001-457603/49. P-PSDB; AAM25242. Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

Claim 1; Page 309; 1217pp; English.

AAM25963. The proteins can have activities based on the tissues and cells AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antiheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; antianemic; antiagragant; haemostatic; vulnerary; antianemic; antiagragant; haemostatic; vulnerary; antianemic; antiagragant; haemostatic; vulnerary; antidabetic; cytostatic; neuroprotective; antidapressant; noofropic; antidabetic; cytostatic; neuroprotective; antidapressant; noofropic; antidabetic; cytostatic; neuroprotective; antidepressant; noofropic; antidabetic; cytostatic; neuroprotective; antidepressant; noofropic; contingation the new proteins and polymucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polymucleotides are useful for screening for agonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, cardiac anaphylaxis, viral, anaemia, alleraic anaphylaxis, amminish, wounds, butterial, lergia. anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Aliheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders

Sequence 519 BP; 101 A; 169 C; 160 G; 89 T; 0 U; 0 Other;

Gaps ö 87.3%; Score 316.8; DB 4; Length 519; 99.4%; Pred. No. 8.7e-77; tive 0; Mismatches 2; Indels 0. Query Match Best Local Similarity 99.4³ Matches 318; Conservative

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9 1 ATGGTGGTAGTCACGGGGGGGGGGAGCCAGACAGCGGTCAGGACGGTGCCATGTCCAGC

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crythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus)

cr imyeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia)

cr i wounds, ulcers, burns; bone disorders (e.g. osteoporosis,

cretama, ilung or liver fibrosis, reperfusion injury in various tissues;

cr trauma); lung or liver fibrosis, reperfusion injury in various tissues;

cr allergic rhinitis, asthma; coagulation disorders (e.g. septic shock,

cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's

cr allergic rhinitis, asthma; coagulation disorders (e.g. septic shock, Crohn's

cr allergic rhinitis, and inflammatory diseases (e.g. septic shock, Crohn's

cr and tumours; and inflammatory diseases (e.g. septic shock, Crohn's

cr disease, anaphylaxis). The protein may be used to inhibit the growth,

cr disease, anaphylaxis). The protein may also have

cr diffection or function of infections agents such as bacteria, fungi,

cr rifection or function is the may also have

cr differation/differentiation, stem cell growth factor, haematopoiesis

crequlation, immune stimulating or suppressing, chemotactic/chemokinetic,

haemostatic and thrombolytic, receptor/ligand, and antiinflammatory

cr combinant protein for analysis. The present sequence represents a novel-

cr combinant protein for analysis. The present sequence is an expressed

cr human cDNA sequence of the invention, this sequence is an expressed

cr human cDNA sequence of the invention, this sequence is an expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hundington's disease, amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; parkinson's disease, Alzheimer's disease; neurodegenerative disease; parkinson's disease; Alzheimer's disease; autoimmune disease; systemic lupus erythematosus; rheumatoid arthitis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoprosis; osteoarthritis; stroke; librosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; cronn's disease; anaphylaxis; profiferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemokinetic; haemostatic; antinflammatory; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
                                                                                                                                                                 240
                                               188
                                                                                                                                                                                                                                            TTCAGTGGGGGGCACTACATCCCCACGGACTCCGAGGGCCGGTACTTCATCGACCGAGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. systemic lupus
                               GGGCTGCCCCTGCCTGCCACAGGAGTTTCCTGAGGTTGTTTCCCCTTAACATCGGAGGGCT
                                                                                                                                                                                      CACTICACTACACGCCTGTCCCACACTGCGGGGGCTACGAAGACACCATGTTGGCAGCCATG
                                                                                                                                                                                                                                                                      TTCAGTGGGGGGCACCACTACATCCCCACGGACTCCGAGGGCCGGTACTTCATCGACCGAGAT
                                                                                                                                                                 CACTTCACTACACGCCTGTCCACACACGGGGGGCTACGAAGACACCATGTTGGCAGCCATG
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Drmanac RT;
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Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang TY, Liu C, Zhou P, Asundi V,
Kue AJ, Yang Y, Wehrman T, Wang J,
                                                                                                                                                                                                                                                                                                                          GGCACACACTTTGGGTATGT 320
                                                                                                                                                                                                                                                                                                                                                               GGCACACACTTTGGAGATGT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human cDNA sequence #405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX71180 standard; cDNA; 1068
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0
                                                                                                                                 Score 316.8; DB 7; Length 1068;
Pred, No. 1e-76;
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Sequence 1068 BP; 209 A; 321 C; 325 G; 213 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  Indele
                                                                                                                                                                                                                                                                                  7
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                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 318; Conservative
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This sequence represents the CDNA for a human immune system molecule (IMO1) isolated as clone 2751129 from the Incyte THP1AZS08 library. The human IMMO1s (ABAB1535-B15550) and their encoding polymuclectides (AAA95775-A95789), and compositions comprising polymuclectides (AAA95775-A95789), and compositions of immunological disorders, infections diagnosis, treatment or prevention of immunological disorders, infections and cell proliferative disorders, including cancer. The IMOL may be used to treat or prevent disorders associated with decreased expression or activity of IMOL, such as immunological disorders (e.g. inflammation, activity of IMOL, such as immunological disorders (e.g. inflammation, activity of IMOL, such as immunological disorders (e.g. inflammation, bacteria (e.g. Staphylococcus, Streptococcus, Shigella), fungi (e.g. bacteria (e.g. Staphylococcus, Streptococcus, Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. plasmodium, Trypanosoma, intestinal protozoa), cell proliferative disorders (e.g. actimic certenoma, sarcoma), cell proliferative disorders (e.g. actimic development of antibodies that specifically recognizes these peptides. The polymuclectides may be used to detect and quantify game expression in disease, as targets in a microarray, to detect differences in gene capening libraries of compounds in drug screening techniques. Antibodies which specifically bind to IMOL may be used for the diagnosis of minibitors of any activity of any sexpension of IMOL, or in assays to monitor of interests being treated with IMOL or agonists, or inhibitors
                                                                                                                                                                                                                                                                                        New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
                                                                                                                                                                           Azimzai Y,
                                                                                                                                                                               Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 88; 95pp; English.
                 04-APR-2000; 2000WO-US009072
                                                               99US-0127852P
                                                                                                                                                                               Lal P, Tang YT,
                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                           WPI; 2000-665005/64.
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                                                               05-APR-1999;
05-MAY-1999;
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Sequence 1124 BP; 227 A; 319 C; 343 G; 233 T; 0 U; 2 Other;

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Match 87.3%; Score 316.8; DB 3; Length 1124; Local Similarity 99.4%; Pred. No. 1.1e-76; les 318; Conservative 0; Mismatches 2; Indels 0;
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1 ATGGTGGTAGTCACGGGGGGGGGGGAGCCAGGCGGTCGTCAGGACGGTGCCATGTCCAGG 108 ATGGTGGTAGTCACGGGGCGGGAGCCAGACAGCCGTCGTCAGGACGGTGCCATGTCCAGC 61 TCTGACGCCGAAGACGACTTTCTGGAGCCGGCCGACGCCGACGGCCACGCCACG 168 TCTGACGCCGAAGACGACTTTCTGGAGCCGGCCACGCCGACGGCCACGCCAGGCGGGGCAC

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240 347

288 CACTICACTACACGCCIGTCCACACTGCGGTGCTACGAAGACACCATGTIGGCAGCCATG

181

228 GCGCTGCCCTGCTGCCACAGGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGCCT CACTTCACTACACGCCTGTCCACACTGCGGGGCGAAGACACACCATGTTGGCAGCCATG

121 GCGCTGCTGCTGCCACAGGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGGCT

180

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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynuclectides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                    Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-ADAS4041). The coding sequences are useful in the gene therapy of diseases caused by aborealities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1045; 205pp; English.
                                                                                                                                                                                         Human coding sequence, SEQ ID 1045.
328 GGCACACTTTGGAGATGT 347
                                                                                             85
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                             ADA53477 standard; cDNA; 2576
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                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                             (first entry)
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                             20-NOV-2003
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                                                                                                                             ADA53477;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Since: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                281 ccacedacreceassacederacricaredacedadarescacacacarrisesiarere 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe; 88
                                 141 CACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATGTTCAGTGGGGCGCACTACATCC
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                                                                                                                                                                                                                              CTCCCTCTACAATCAACTTTGTAGTCCTAGCAGGTGATTAG 363
                                                                                                                                                                                                                                                         CTCCCTCTACAATCAACTTTGTAGTCCTAGCAGGTGATTAG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0207456P.
2000US-0060840B.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA53148 standard; DNA; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483447/52
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002
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203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 TOGAGCCGGCCACGCCGACGCCACGCAGGCGGGCACGCGCTGCCCCTGCTGCCACAGG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 ideadececededence de antico de contra de la reconsta del reconsta de la reconsta de la reconsta del reconsta de la reconst
   The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. Notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #1411 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 473 BP; 131 A; 112 C; 111 G; 119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.1%; Score 221.8; DB 4; Length (86.8%; Pred. No. 7.9e-51; ive 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 1411; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR
                                                                                         GGCACACACTTTGGGTATGT 320
                                                                                                                        GGCACACACTTTGGAGATGT 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312P.
2000US-0207456P.
2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                              AAI11478 standard; DNA; 473
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                   AAI11478;
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                                                                                                                                                                                                                                    RESULT 6
AAI11478/c
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282
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                                            CACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATGTTCAGTGGGCGGCACTACATCC 262
                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
CACTGCGGTGCTACGAAGACACCATGTTGGCCATGTTTCAGTGGGCGGCACTACACTCC
                                                                                                                                                                                                                                                                                                                                             Probe #1439 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 473 BP; 131 A; 112 C; 111 G; 119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.1%; Score 221.8; DB 4; Length 9 Best Local Similarity 86.8%; Pred. No. 7.9e-51; Matches 244; Conservative 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
                                                                                                                                                          CTCCCTCTACAATCAACTTTGTAGTCCTAGCAGGTGATTAG 363
                                                                                                                                                                          CTCCCTCTACAATCAACTTTGTAGTCCTAGGAGGTGATTAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 1439; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                           AAI32753 standard; DNA; 473 BP
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30-UTN-2000; 2000US-0060840B
03-MDC-2000; 2000US-0063366
21-SEP-2000; 2000US-023466PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312P.
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                  401
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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 calls. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from meRNA channers. The method involves contacting the from mRNA channers. The probes are useful for verifying the cxpression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional microarrays from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this nucleic acid probe of the printed specification, but was obtained
322
                                                                                           281 CCACGGACTCCGAGGGCGGTACTTCATCGACCGAGATGGCACACTTTGGGTATGTCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; microarray; single exon probe; gene expression; breast; disease;
                                                                          CCACGGACTCCGAGGGCCGGTACTTCATCGACCGAGATGGCACACACTTTGGGTATGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1415; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                   Human breast cell single exon mucleic acid probe #1415
                                                                                                                                              CTCCCTCTACAATCAACTTTGTAGTCCTAGCAGGTGATTAG 363
                                                                                                                                                                     CICCCTCTACAATCAACTTTGTAGTCCTAGCAGGTGATTAG 181
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                                                                                                                                                                                                                                  RESULT 9
ABA42720/c
ID ABA42720 standard; DNA; 473 BP.
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26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00603408.
03-AUG-2000; 2000US-00532366.
21-SEB-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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83 TEGRACICEGCCACGCCGACGCCACGCAGGCGGGCACGCCTGCTGCTGCTGCCACAGG 461 ricia accicio de contra en contra de contr

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Wang, Jian-Wang
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                                                                                                                                                                                                                                                                June 8, 2004, 09:16:13 ; Search time 84 Seconds (without alignments) 2398.181 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-024-579-4
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1 atggtggtagtcacggggcg......tagtcctagcaggtgattag 363
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1. \c9T2_6\ptodata/2\ina\5A_\comB.seq:*
2. \c9T2_6\ptodata/2\ina\5B_\comB.seq:*
3: \c9T2_6\ptodata/2\ina\6A_\comB.seq:*
4: \c9T2_6\ptodata/2\ina\6B_\comB.seq:*
5: \c9T2_6\ptodata/2\ina\PcTUS_\comB.seq:*
6: \c9T2_6\ptodata/2\ina\PcTUS_\comB.seq:*
6: \c9T2_6\ptodata/2\ina\PcTUS_\comB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-316-643A-24
US-09-316-643A-21
US-09-316-643A-21
US-09-316-643A-21
US-09-316-643A-11
US-09-312D-1058
US-09-312D-1058
US-09-252-991A-3218
US-09-252-991A-3218
US-09-252-991A-4718
US-09-252-991A-4718
US-09-252-991A-4718
US-09-252-991A-4755
US-09-252-991A-4775
US-09-252-991A-4775
US-09-252-991A-1589
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-621-976-16656
US-09-252-991A-2363
US-09-252-991A-2363
US-09-621-976-16656
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US-09-252-991A-2363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                         - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Query
Match Length DB
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Perfect score: 3
Sequence: 1
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2 US-08-997-080-185 Sequence 185, App 2 US-08-997-362-185 Sequence 185, App 4 US-09-205-855-185 Sequence 185, App 4 US-09-205-426-185 Sequence 185, App 4 US-09-205-855-204 Sequence 204, App 4 US-09-205-426-204 Sequence 204, App 5 US-09-205-426-204 Sequence 204, App 6 US-09-205-914A-260 Sequence 204, App 7 US-09-103-840A-1 Sequence 2, Appli 8 US-09-103-840A-1 Sequence 6, Appli 8 US-09-26-901A-624 Sequence 604, Appli 8 US-09-26-901A-604 Sequence 604, Appli 8 US-09-26-901A-604 Sequence 604, Appli 9 US-09-489-039A-3869 Sequence 3, Appli 1 US-07-642-734C-3 Sequence 3, Appli 1 US-07-642-734C-3 Sequence 3, Appli	ALIGNMENTS	uS/09621976 warde, J.B. and Encoded Human Proteins. 4PR2 R: US/09/621,976 00-07-21	.6%; Score 49.2; DB 4; Length 318; .0%; Pred. No. 0.00012; e 0; Mismatches 53; Indels 1; Gaps 1;	ATCGAGGGGTCACTTCACTACACGCCTGTCCACACGCGGTGCTACGAAGACACCATG 228	ACACTTIGG 314 GCACTTIGG 292	US/09336643A W P. Edward
9.1 898 9.1 898 9.1 898 9.1 1164 9.1 1164 9.1 1164 9.1 1150 9.0 4403765 9.0 4403765 9.0 1506 9.0 1506 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 1605 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0		ication illue Ed illue Ed illue Ed in c, u. v. in c, u.v. in ESTS in E	larity 63 Conservativ	TGGAGGGGTCAC 	ATCGACCGAGATGGCACACACTTTGG	plication 1761 TION: ler, Andre rran, Mark r. Ping t.er, Marc
		RESULT 1 US-09-621-976-1336 Sequence 1335, Appl Patent No. 6639063 GENERAL INFORMATION PERFICANT: JOBERT PPPLICANT: GLOCHER TITLE OF INVENTON FILE REFERENCE: GE CURRENT FILING DAT CURRENT FILING DAT NUMBER OF SEQ ID N SOFTWARE: Patent. p SEQ ID NO 1336 LENGTH: 318 TYPE: DAA ORGANISM: Homo Sa; FEANTRE: NAME/KRY: CDS NAME/KRY: CDS FEANTRE: NAME/KRY: CDS FEANTRE: COCATION: 33.31	Query Match Best Local Simi Matches 92;	169 ATC 148 ATC 229 TTC		\$ 2 2 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
13.3%; Score 48.4; DB 4; Length 1542;
Best Local Similarity 54.5%; Pred. No. 0.00032;
Matches 97; Conservative 0; Mismatches 81; Indels 0;
FILE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REPERENCE: SEG-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: 90-119
PRIOR APPLICATION NUMBER: POT/US99/03826
PRIOR FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LIBNGTH: 1542
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APPLICANT: Willer, Andrew P.
APPLICANT: Willer, Andrew P.
APPLICANT: Miller, Andrew P.
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Warc
APPLICANT: Warc
APPLICANT: Wars
ITILE OF INVENTION: No. 6399761el Human Potassium Channels
ITILE OF INVENTION NUMBER: 60/006,687
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR APPLICATION NUMBER: PCT/US99/03826
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PASSER for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1751
TYPE: DNA
PRIOR H. Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEX: CDS
LOCATION: (88)...(799)
CTHER INFORMATION: K+Hnov28, splice 4
US-09-336-643A-24
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| NAME/KBY: CDS
| LOCATION: (297)...(1008)
| OTHER INFORMATION: K+Hnov28 splice 3
US-09-336-643A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-09-336-643A-23
Sequence 23, Application US/09336643A
Patent No. 6399761
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: H. sapiens
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Best Local Similarity
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144 GTTTCTGAGGTTGTTCCCCTTAACATCGGAGGGCTCACTTCACTACACGCCTGTCCAC 203
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-336-643A-21

### Sequence 21, Application US/09336643A

### Patent No. 6399761

### APPLICANT: Miller, Andrew P.

### APPLICANT: Miller, Andrew P.

### APPLICANT: Miller, Mark Edward

### APPLICANT: Wang, Jianwang

### APPLICANT: Wang

### APPLICA
     81; Indels
     0; Mismatches
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LOCATION: (346)...(1057)

OTHER INFORMATION: K-HNOV28, splice 1

US-09-336-643A-21
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Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Willer, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Reter, Marc
     97; Conservative
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ORGANISM: H. sapiens
FRATURE:
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Matches
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Rubanited (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Rubanited (OCT-200
61 HFTTRLSTLRCYEDTMLAAMPSGRHYIPTDSBGRYFIDRDGTHFGDV----LNP-LRSGD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTINFVVLAGD 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLING=223546683; PubMed=12466851;
The FANYOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AA; 33132 MW; IPODIF618CD5E459 CRC64;
                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ32069.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                        289 AA
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                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA FLJ32069 FIS.
9430010P06RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8C0S7
Q8C0S7;
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08COS7
10 08COC
AC 08COC
DT 01-M
DT 0
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RC STRAIN=CS7BL/6J; TISSUE=Body;

RC STRAIN=CS7BL/6J; TISSUE=Body;

RC STRAIN=CS7BL/6J; TISSUE=Body;

RA MEDINE=ZS346693; PubMed=12466851;

RA The FANTOM Consortium,

RA The FANTOM Consortium,

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of

RT "Analysis of the mouse transcriptome based on functional annotation of

RT "Analysis of the mouse transcriptome based on functional annotation of

RT "Analysis of the mouse transcriptome based on functional annotation of

RT "Analysis of the mouse transcriptome based on functional annotation of

RG OF GO:00058193; Proflessium channel complex; IEA.

DR GO; GO:0005515; Proclean binding; IEA.

DR GO; GO:0005515; Proclean binding; IEA.

DR GO; GO:0005519; Procleasium ion transport; IEA.

DR GO; GO:0005313; Refera; I.

REPPRO; IRRO00210; BTB_POZ.

DR InterPro; IRRO002113; Ktetra; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HFTTRLSTLRCYEDTMLAAMPSGRHY1PTDSEGRYFIDRDGTHFGYVSPSTINFVVLAGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HFTTRLSTLRRYEDTWLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDV----LNF-LRSGD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTINFVVLAGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVVVIGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEPPEVVPLNIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVVVTGREPDSRRODGAMSSSDABDDFLEPATPTATQAGHALPLLPQEFPBVVPLNIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                    60,770 full-length cDNAs.";

Nature 420:563-573(2002).

EMGL, AK029942.

MCD; MCI:444226; 943-0010006Rik.

GO; GO:0016020; C:membrane; IEA.

GO; GO:00080515; F:proctein binding; IEA.

GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.

GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

84.1%; Score 530.5; DB 11; Length 239;
Best Local Similarity 87.5%; Pred. No. 1e-49;
Matches 105; Conservative 4; Mismatches 6; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Score 530.5; DB 11; Length 289; llarity 87.5%; Pred. No. 1.3e-49; Conservative 4; Mismatches 6; Indels 5;
                                                                                                                                                                                                                                                                                                      InterPro; IPR001210; BTB POZ.
InterPro; IPR001311; K tetra.
Pfam: PF02214; K tetra; 1.
SMART; SM00225; FTB; 1.
SRQUENCE 239 AA; 27173 MW; A889D2E9CBCE528A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PP02214; K tetra; 1.
SMART; SM00225; BTB; 1.
SEQUENCE 289 Aa; 33079 MW; 64263FAZAD19FC2F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2003 (TYEMBLE). 23, Created)
01-WAR-2003 (TYEMBLE). 23, Last sequ
01-007-2003 (TYEMBLE). 25, Last anno
CDNA FLJ23069 FIS.
9430010P0G6RIK.
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01-MAR-2003
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7

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June Run on:

8, 2004, 10:14:29; Search time 79 Seconds (without alignments) 479.268 Million cell updates/sec

US-10-024-579-5

631 1 MYVVTGREPDSRRQDGAMSS.....GTHFGYVSPSTINFVVLAGD 120 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 Total number of hits satisfying chosen parameters:

1017041 seqs, 315518202 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPIREMBL

sp arches:*
sp bacteria:*
sp buman:*
sp human:*
sp invertebrate:*
sp marmal:*
sp mhc:*
sp phage:*
sp phage:*
sp plant:*
sp_plant:*
sp_credent:*

sp_virus:*
sp_vertebrate:*
sp_unclassified:* rvirus:*
bacteriap:*

sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Q	Description	Q8ivr0 homo sapien Q96mg8 homo sapien Q80087 mus musculu Q8b1k1 mus musculu Q86ca93 mus musculu Q80ca9 mus musculu Q8bc74 mus musculu Q9bc68 macaca fasc Q8cb6 macaca fasc Q9bc68 macaca fasc Q9bc68 macaca fasc Q8bc76 mus musculu Q9vdh3 drosophila Q8tca6 homo sapien Q8tbs6 homo sapien Q8bby7 mus musculu Q8bby7 mus musculu Q8bby7 mus musculu Q8bby7 mus musculu
COLUMN		88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Ď	£	QBIVRO QBENTRO QBCGST QBCAA3 QBCAA3 QBCAA3 QBCBRCO QBCBRCO QBCBRCO QBCCBC QBCCBC QBCCBC QBCCBC QBCCCBC QBCCCBC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC QBCCCAC
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	* Query Match Length DB	2888 2889 3869 22288 3223 3233 301
	* Query Match	222333355000000000000000000000000000000
	Score	5000 5000 5000 5000 5000 5000 5000 500
	Result No.	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

Q8nc69 homo sapien Q96a1 homo sapien Q8x219 homo sapien Q7t22 rattus norv Q922M3 mus musculu Q9p2M9 homo sapien Q9h216 homo sapien Q8c004 mus musculu Q96p31 homo sapien Q8c004 mus musculu Q96p31 homo sapien Q9hq6 oryza sativ	QBewin2 homo sapien Q7tnyl rattus norv Q7tnyl rattus norv Q86cbq wus musculu Q96cx2 homo sapien Q8ff1 echistosoma Q70479 wus musculu Q8vxf5 homo sapien Q9cyx4 wus musculu Q9cyx1 mus musculu Q9cx3 mus musculu Q9cx3 mus musculu Q9cx3 mus musculu Q9cx3 mus musculu Q8cx3 mus musculu Q8cx3 mus musculu Q8cx1 mus musculu Q8cx1 mus musculu Q8cx0 mus musculu
08NC69 096SA1 08WZ19 08T024 095ZW3 099ZW9 099EW9 096T91 08CD04 09CD04 09CD04	Q8WUNZ Q7TNY1 Q7TNY1 Q96CX2 Q86FF1 O70479 Q88XX5 Q8WVPS Q9D7X1 Q9D7X1 Q9D7X1 Q9D7X1 Q8CQ3 Q8KOB1
44414144444 101 1 1 0 0	4114611411411
2222 4 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	22 24 25 25 25 25 25 25 25 25 25 25 25 25 25
00000000000000000000000000000000000000	22222222222222222222222222222222222222
140.5 140.5 140.5 140.5 139.5 138.5 138.5 138.5 132.5 132.5	130 129.5 127.5 127.5 126.5 125.5 125 125 125 125 124 127
33 22 23 24 3 24 24 24 24 24 24 24 24 24 24 24 24 24	0.000000000000000000000000000000000000

ALIGNMENTS

5; Gaps Query Match 88.8%; Score 560.5; DB 4; Length 288; Best Local Similarity 91.7%; Pred. No. 6.8e-53; Matches 110; Conservative 3; Mismatches 2; Indels 5;

3

ò 日 ઠે SECUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                      53 VPLNIGGAHPTIRLSTLRCYEDIMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG----YVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                           EMBL; M60783; AAA58385.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND TISSUS SPECIFICITY.

TSSUSEMBEDTYONIC Kidney;

MEDLINE=20195625; PubMed=10729221;
Isbrandt D., Leicher T., Waldschuetz R., Zhu X.-R., Luhmann U.,

Michal U., Sauter K., Pongs O.;

"Gene structures and expression profiles of three human KCND (Kv4)

potassium channels mediating A-type currents I(TO) and I(SA).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCD1 HUMAN STANDARD; PRT; 647 AA.
OSNSEA, 075671.
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Potassium voltage-gated channel subfamily D member 1 (Potassium channel Kv4.1).
                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                           19.9%; Score 125.5; DB 1; Length 316; 48.4%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                                            D20B810A00507DCF CRC64;
                                                                                                                                                                                                                                                                                                                                                      48.4%; Pred. no. +ive 7; Mismatches
                                                                                                                                                                                                MIM; 191161; -.
InterPro; IPR00210; BTB_POZ.
InterPro; IPR003131; K_tetra.
Pfam; PF02214; K_terra; I.
SMART; SM00225; BTB; I.
PROSITE; PS50097; BTB; I.
                                                                                                                                         EMBL; AY065346; AAL38649.1; -. EMBL; BC001643; AAR01643.1; -. EMBL; BC001949; AAR01949.1; -. Genew; HGNC:11894; INFAIP1.
                                                                                                                                                                                                                                                                                                            SEQUENCE 316 AA; 36204 MW;
                                                                                                                                                                                                                                                                                                                                                                        31; Conservative
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                       EMBL;
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REAUTINE-2238825; PubMed=12477932;

RY SURJUNE-2238825; PubMed=12477932;

RY STRAUMINE-2238825; PubMed=12477932;

RA Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G., Shuller G.D.,
Altschul S.P., Zebeng B., Buetow K.H., Schaefer C.F., Batk N.K.,
Altschul S.P., Zebeng B., Buetow K.H., Schaefer C.F., Batk N.K.,
RA Bachul S.P., Logical Jan M., Peters G.J., Rang G.M., Holp L.,
Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bratchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Bratchenko L., Marusina K., Poshiyuki S., Carminci P., Prange C.,
Raba S.B., McEwan P.J., McKernan K.J., Abramon R.D., Millahy S.J.,
Rabas S.A., McEwan P.J., McKernan K.J., Madan A., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulks S.W.,
Rahy J., Helton E., Retream M., Madan A., Rodrigues S., Sanchez A.,
Rahy J., Helton E., Retream M., Green E.D., Dickson M.C.,
Rabas Bakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
Rabas Bakesley R.W., Schmitz J. M., Marza M.A.,
Butterfield Y.S.N., Krzywinski M.I., Skalsku U., Smailus D.E.,
Rodriguez A.C., Grimwood J., Schmutz J. Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J. Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J. Myers R.M.,
Rabas R.M., Schain J. E., Jones S.J.M., Marza M.A.,
Rabas R.M., Schain J. E., Jones S.J.M., Marza M.A.,
R. Generation and initial analysis of more than 15,000 full-length
R. G. Current in heart and I (3s) current in neurons. Channel properties
are modulated by interactions with other alpha subunits and with
regulatory subunits.
C. I. Subgillarity).
Associates with the regment A. is probably the voltage-sensor and is
in particular in neurons.
In particular in neurons.
In particular in neurons.
In Substituty Resignes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIN; 300281;

R GO; GO:0005249; F:voltage-gated potassium channel activity; NAS.
R GO; GO:0005249; F:voltage-gated potassium channel activity; NAS.
R GO; GO:0005249; F:voltage-gated potassium channel activity; NAS.
R InterPro; IPR005821; Ion_trans.
R InterPro; IPR005821; Ion_trans.
R InterPro; IPR004054; KY4channel_Dore.
R InterPro; IPR003966; KY channel.
R InterPro; IPR003911; K_channel.
R InterPro; IPR005820; M+channel_nlg.
R InterPro; IPR005820; M+channel_nlg.
R InterPro; IPR005820; M+channel_nlg.
R InterPro; IPR00520; ion_trans; 1.
R Pfam; PF00520; ion_trans; 1.
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EMBL; AF166006; AAF65517.1; -.
EMBL; AF166006; AAF65617.1; JOINED.
EMBL; AF166005; AAF65617.1; JOINED.
EMBL; AB021865; BAA96451.1; -.
EMBL; A005899; CAA06755.1; -.
EMBL; AC045659; AA445659.1; -.
AF8F; OZ7564; 1LNQ.
Genew; HGNC:6237; KCNDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0169; KCHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily.
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TISSUB=Heart;
Makita N., Shirai N., Sawa H., Sasaki K., Nagashima K., Yoshida M.C.,
Kitabatake A.; "Homo sapiens mRNA for shal-type potassium channel KCND1 (Kv4.1)."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

Genomics 64:144-154 (2000).

SEQUENCE FROM N.A.

Strom T.M., Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,

SEQUENCE FROM N.A.

rissum=Brain; Meindl A.;

"Transcription map in Xp11.23."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. [4]

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

June 8, 2004, 10:12:49; Search time 39 Seconds (without alignments) 160.216 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-024-579-5 631 1 MVVTGREPDSRRQDGAMSS.....GTHFGYVSPSTINFVVLAGD 120

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* **Database**:

Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	29 homo	homo	uns o	Q14681 homo sapien		Q9ukl7 homo sapien	_	Q9ttt5 oryctolagus		_						-	_	Q63881 rattus norv				P10499 rattus norv	mue n			P22739 xenopus lae		P16390 mus musculu			рошо	P49916 homo sapien	Bacc
SUMMARIES		a		KCD1_HUMAN	KCD1 MOUSE	Y176 HUMAN	CIKS_RAT	KCD3 HUMAN	KCD3_MOUSE	KCD3_RABIT	KCD3_RAT	CIKS_DROME	CIKS_MOUSE	CIKS HUMAN	CIKI DROME	CIK2_HUMAN	KCD2_HUMAN	KCD2_MOUSE	KCD2_RABIT	KCD2_RAT	CIK3_RAT	NCR2 HUMAN	CIK1_MOUSE	CIK1_RAT	CIK2_MOUSE	CIKLHUMAN	CIK3_HUMAN	CIK2 XENLA	CIKS MUSPF	CIK3_MOUSE	CIK6_HUMAN	CIKS_RABIT		DNL3_HUMAN	RRN6_YEAST
		80	п	-	ч	Н	Н	Н	-	Н	H	Н	н	Н	Н	н	н	н	-	-	H	-	H	-	-	-	-	~	-		H	~	-	**1	-
		Match Length	316	647	651	265	602	655	655	655	655	959	602	613	490	499	630	630	630	630	525	2517	495	495	499	495	523	499	601	528	529	598	653	922	894
•	8	Match	19.9	15.6	15.6	14.4	14.0	13.5	13.5	13.5	13.5	13.5	13.4	13.2	13.1	13.1	12.8	12.8	12.8	12.8	12.5	12.5	12.4	12.4	12.4	12.3	12.0	11.8	11.8	11.6	•	•	٠	11.2	11.0
		Score	. 5	98.5	98.5	91	88.5	82	82	85	85	85	84.5	83.5	82.5	82.5	81	81	81	81	79	79	78.5	78.5	78.5	77.5	16	74.5	74.5	73	73	72	73	70.5	
	T (USA)	No.		7	m	4	w	9	7	80	6	10		12	13	14	15	16	17	18	19	20	21	22	53	24	25	26	27	28	29	. 30	ed 60	35	33

		P39684 Baccharomyc Q28527 mustela put Q91sv5 sus scrofa Q9wu42 mus musculu D1764 mattus morv	
SUL1_DROME ORC2_DROME DMSA_HAEIN	PO51_BOVIN CIK4_MOUSE AXN2_BRARE TX18_MOUSE	PES4_YEAST CIX4_MUSPP PO51_PIG NCR2_MOUSB	TW-WID
ннн			1
1114 618 806	360 654 812 613	611 654 360 2472	e e
10.0	0.01	7.01 7.01 7.01 7.01 7.01	9
69 69 69	ស ស ស ស ស ស ស ស ស ស	67.5 67.5 67.5	0
	6 8 8 9 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ņ

ALIGNMENTS

A; Introns: 131/1

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potassium channel protein A (clone Sh-beta) - fruit fly (Drosophila melanogaster) C.Species: Drosophila melanogaster C;Dsc: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000 C;Accession: 800480, 801111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-670 cABA;
A;Cross-references: EMBL;AF022982; PIDN:AAB69932.1; GSPDB;GN00023; CESP:T23B12.6
A;Experimental source: strain Bristol N2; clone T23B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Mus musculus (house mouse)
C; Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999
C; Accession: A39372
C; Accession: A39372
C; Accession: A39372
E; Park, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salkoff, L.
Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991
A; Title: mShal, a subfamily of A-type K(+) channel cloned from mammalian brain.
A; Reference number: A39372; WUID:91239573; PMID:2034678
20 ERVLANVGGKKPETTVATLTRVSDTVLAVMVSDRW--KTGDE--IFIDRDPKHPGKVLNY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LPLAQQPLPPAPBUKASRGDBVLVVNVSGRRFETWKNTLDRYPDTLLGS--SEKBFYDA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 LPLLPQEPP-----EVVPLNIGGAHFTTRLSTLRCYEDIMLAAMFSGRHYIPTD 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T23B12.6 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 29-Oct-1999 #text_change 29-Oct-1999 C; Accession: T32221 R; Pavidson, S.; Wohldmann, P.; Gillam, B. R; Davidson, S.; Wohldmann, P.; Gillam, B. A; Description: The sequence of C. elegans cosmid T23B12. A; Reference number: Z21137 A; Reference number: Z21137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Molecule type: mRNA
A;Residues: 1.651 <PAK>
A;Cross-references: GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
15.6%; Score 98.5; DB 2; Length 651;
Best Local Similarity 33.3%; Pred. No. 0.027;
Matches 28; Conservative 10; Mismatches 29; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 IVNIAVGGRIPATSCNTLTWIPDSFFTSLLSGRANSVXDPSGAIPIDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 87/2; 185/3; 293/1; 400/1; 457/1; 540/2; 635/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 SEGRYPIDRDGTHFGYVSPSTINF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potassium channel protein Shall - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESGEY FPDRDPDMFRHV----LNF
                                                                                                                                                                                 106 -----YVSPS 110
                                                                                                                                                                                                                                                                                                86
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76 LRDGDHFVAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: T23B12.6
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Type the circal protein F18A11.5 - Caenorhabditis elegans
Cypotherical protein F18A11.5 - Caenorhabditis elegans
Cypotherical canorhabditis elegans
Cypother: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Cypotession: Tizees
Rywallis, J.
Submitted to the EMBL Data Library, October 1998
AyAccession: Tizees
AyAccession
                                                                                                                                                                                                                                                                                                                                    51 BVVPLNIGGAHFTTRLSTLRCYEDTWLAAMFSG-----RHYIPTDSEGRYFIDRDGTHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dypotherical protein D2045.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2036
C;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 EVVPLAIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSBGRYFIDRDGTHFG---- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LEPATPTATQAGHALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMEAAMFSGRHYI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 DVITLANGGTMYTTTRSTLSKETDTLLANIASGSLSEDEQANVTLPDGTLFVDRDGPLF
                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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16.4%; Score 103.5; DB 2; Length 373;
Best Local Similarity 42.3%; Pred. No. 0.0041;
Matches 30; Conservative 6; Mismatches 20; Indels 15;
                                                                                                  Query Match 17.6%; Score 111; DB 2; Length 190; Best Local Similarity 41.3%; Pred. No. 0.0003; Matches 26; Conservative 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
16.8%; Score 106; DB 2; Length 220
Best Local Similarity 31.8%; Pred. No. 0.0012;
Matches 28; Conservative 12; Mismatches 24; Indels
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88 PTDSEGRYFIDRDGTHFGYVSPSTINFV 115 : || : || || || : : || : 41 TKNEEGSVFIDRDSKHFRLI----LNFL 64

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A;Map position: 3 A;Introns: 39/3; 127/3; 169/1; 194/3

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A;Gene: CESP:F18A11.5 A;Map position: 2 A;Introns: 7/3; 44/3; 99/3; 152/2; 198/3; 223/1

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 8, 2004, 10:42:29; Search time 45 Seconds (without alignments) 256.511 Million cell updates/sec

US-10-024-579-5 631 1 MVVVTGREPDSRRQDGAMSS......GTHFGYVSPSTINFVVLAGD 120

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: Dirl:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	tumor necrosis fac	hypothetical prote	hypothetical prote		potassium channel	hypothetical prote	potassium channel					potassium channel	hypothetical prote		potassium channel	potassium channel	potassium channel	voltage-sensitive	potassium channel					potassium channel	hypothetical prote				potassium channel
		£	A41784	T26019	T20366	T26685	A39372	T32221	S00480	JH0166	JH0193	S02284	C49507	A49507	T27759	\$51212	S21144	A35312	I77466	JU0271	A43531	860255	A40090	B39113	I84204	A33814	T32065	T25973	157680	A56031	A38101
		98	2	N	N	c	N	N	N	N	~	N	~	N	~	7	~	N	N	N	N	N	~	~	~	N	N	N	N	N	0
		Match Length	348	190	220	373	651	670	643	602	656	304	514	602	460	597	476	490	499	630	525	1495	495	495	499	499	134	208	495	613	523
ď	Query	Match	19.9	17.6	16.8	16.4	15.6	14.6	14.3	14.0	13.5	13.4	13.4	13.4	13.2	13.2	13.1	13.1	13.1	12.8	12.5	12.5	12.4	12.4	12.4	12.4	12.3	12.3	12.3	12.3	12.2
		Score	125.5	111	106	103.5	98.5	35	90	88.5	85	84.5	84.5	84.5	83.5	83.5	82.5	82.5	82.5	81	79	79	78.5	78.5	78.5	78.5	77.5	77.5	77.5	77.5	77
	Result	Š.	-	8	m	4	ß	ø	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	29

	hypothetical prote	hypothetical prote	hypothetical prote	potassium channel	hypothetical prote	hypothetical prote	potassium channel	potassium channel	hypothetical prote	hypothetical prote	hypothetical prote	potassium channel	hypothetical prote	sensory transducti	potassium channel
T25976	T31997	G75382	T25977	JH0313	T15820	T32067	A27159	184205	T02345	T32068	T25974	866669	T16580	876133	A39922
0	N	N	N	N	(7)	N	N	N	N	7	ď	N	N	N	0
140	212	167	84	499	272	326	359	528	1791	139	139	598	13055	222	653
12.1	12.0	11.9	11.8	11.8	11.7	11.6	11.6	11.6	11.5	11.4	11.4	11,4	11.3	11.3	11.3
76.5	26	75	74.5	74.5	74	73.5	73	73	72.5	72	72	72	71.5	71	11
30	31	32	33	34	35	36	37	38	ტ. ტ.	40	41	42	43	44	45

ALIGNMENTS

, V.M.		
RESULT 1 A41784 tumor necrosis factor-alpha-induced protein B12 - human C;Species: Homo sapiens (man) C;Date: 31-Dec-1933 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997 C;Date: 31-Dec-1933 #sequence revision 31-Dec-1993 #text_change 29-Aug-1997 C;Date: 31-Dec-1993 A;Dec-1000	Query Match Best Local Similarity 48.4%; Pred. No. 1.9e-05; Matches 31; Conservative 7; Mismatches 21; Indels 5; Gaps 2; Qy 53 VPLNIGGAHFTTRLSTLRCYBDYMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVS 108	Oy 109 PSTI 112 Db 121 DDTI 124

hypothetical protein VM106R.1 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Pacession: T26019 R.Barlow, K. R.Barlow, K. A.Reference number: 220135 A.Accession: T26019 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Status: preliminary; translated from GB/EMBL/DDBJ A.Status: a.1-190 *WILLs A.Status: 1-190 *WILLs A.Cross-references: EMBL:AL031266; PIDN:CAA20329.1; GSPDB:GN00020; CESP:VM106R.1

C;Genetics: A;Gene: CESP:VM106R.1 A;Map position: 2

```
US-10-086-156-12
US-10-086-156-12
Sequence 12, Application US/10086156
FUBLICATION NO. US20030054989A1
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-S:
TITLE OF INVENTION: K-betaM4 and K-betaM5
TITLE OF INVENTION: WHOBER: US/10/086,156
CURRENT APPLICATION NUMBER: US 60/272,190
PRIOR PEPLICATION NUMBER: US 60/272,190
PRIOR PEPLICATION NUMBER: US 60/274,258
PRIOR APPLICATION NUMBER: US 60/274,258
PRIOR PRIOR PILING DATE: 2001-03-07
NUMBER: OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 VPLNIGGAHPTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                           Sequence 1392, Application US/10296115

Publication No. US20040053248A1

GENERAL INCREMATION:

APPLICANT: Hyear Inc

TITLE OF INVENTION:

FILE REFERENCE: 784FCT

CURRENT APPLICATION NUMBER: US/10/296,115

CURRENT FILING DATE: 2002-11-18

FRIOR APPLICATION NUMBER: US99/488,725

PRIOR PLING DATE: 2000-01-21

PRIOR PLING DATE: 2000-01-21

PRIOR PLING DATE: 2000-01-25

NUMBER OF SEQ ID NOS: 1478
             59 GAHFITIRLSTIRCYEDIMLAAMPSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTINFV 115
                                                    102 GKLYTTSLATLTSFPDSMLGAMFSGKMPTKRDSQCNCFIDRDGKVFKYI----LNFL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels 16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.3%; Score 147; DB 12; Best Local Similarity 38.6%; Pred. No. 2.5e-08; Matches 34; Conservative 14; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 PIDSEGRYFIDRDGTHFGYVSPSTINFV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 KRDSQGNCFIDRDGKVFRYI----LNFL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-296-115-1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: homo sapiens
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Sequence 3, Application US/10080980
Sequence 3, Application US/10080980
Sequence 3, Application US/10080980
Sequence 3, Application US/10080980
Sequence 3, Application US-10080980
INTLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL PITIE OF INVENTION: FOLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL STILE OF INVENTION: FOLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBL ITILE OF INVENTION: FOLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBL ITILE OF INVENTE ILLING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,132
PRIOR PELING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10086156
Publication No. US2003005498941
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: Factamia and K+betamis
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING
TITLE OF INVENTION: TABELS 2002-02-28
FRICH APPLICATION NUMBER: US 60/272,190
PRICH FILING DATE: 2001-02-28
PRICH FILING DATE: 2001-02-28
PRICH SPELICATION NUMBER: US 60/274,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVTGREPDSRRQDGAMSSSDAB----DDFLEPATPIATQAGHALPLLPQEFPEVVPLNIG 58
                                                                                                                                                                       50 PEVVPLNIGGAHPTIRLSTIRCYEDTMLAAMF-SGRHYIPTDSEGRYFIDRDGTHFGYV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 PEVVPLANGGAHFTTRLSTLRCYEDTMLAAMP-SGRHYIPTDSEGRYFIDRDGTHFGYV 107
                                                                                                                                                                                                           2 PEIIELAVGGVSYTTTLATILQDKSTLLAELFGEGRDSLAKDSKGRYFLDRDGVLFRYI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PEIIBLANGGVSYTTTLATLLQDKSTLLAELFGEGRDSLAKDSKGRYFLDRDGVLFRYI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                 23.9%; Score 150.5; DB 14; Length 228; 49.2%; Pred. No. 7.6e-09; tive 12; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.6%; Score 149; DB 14; Length 351; Best Local Similarity 34.2%; Pred. No. 2e-08; Matches 40; Conservative 17; Mismatches 40; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Indels
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1 Similarity 49.2%; Pred. No. 7.6e-09;
29; Conservative 12; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Drosophila melanogaster
US-10-080-980-3
                                                                                                               Conservative
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                                                                                     Best Local Similarity
Matches 29; Conserv
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US-10-086-156-2
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US-10-056-884-5
                                                           Query Match
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Best Local
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Sequence 5, Application US/10056884

Publication No. US20030032786A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TRIED OF INVENTION:
FITTLE OF INVENTION:
GENERAL TAPELICATION UNDER: US/10/056,884

GURRENT APPLICATION NUMBER: US/10/056,884

GURRENT PILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: US 60/263,872

PRIOR APPLICATION NUMBER: US 60/269,794

SEQ ID NOS: 73

SOFTWARE: Patentin version 3.0

SEQ ID NO 5

LENGTH: 228

TYPE: PRT

TYPE: PRT

ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7

US-10-296-II5-757

Sequence 757, Application US/10296115

Publication No. US20040053248A1

GENERAL INFORMATION:

APPLICANT: Hyseq Inc.

TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides

TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides

TITLE OF INVENTION: NOWERR: US/10/296,115

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: US99/488,725

PRIOR PILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US99/552,317

PRIOR PILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MYVVTGREPDSRRQDGAMSSDAEDDFLEPATPTATQAGHAL-PLLPQEFPEVVPLNIGG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 96;
                                                                                                                                                                                                                                                                                                                                                                      Score 302.5; DB 14; Length
Pred. No. 9.3e-27;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.9%; Score 220.5; DB 1
78.3%; Pred. No. 3.5e-17;
tive 1; Mismatches 11
                PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.0
SEQ ID NO 39
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.9%;
Best Local Similarity 85.7%;
Matches 60; Conservative
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Best Local Similarity 78.3
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 TINFVVLAGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||:
58 -LNP-LRSGD 65
                                                                                                                                                                                                                  TYPE: PRT
; ORGANISM: homo sapiens
US-10-086-156-39
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; ORGANISM: Homo sapiens
US-10-296-115-757
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Publication No. US2003005499A1
GENERAL INPORMATION:
Paterior No. US2003005499A1
GENERAL INPORMATION:
POLYMORY: Britatol-Myers Squibb Company
TITLE OF INVENTION: POLYMOCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: POLYMOCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: POLYMOCLEOTIDE ENCODING
TITLE OF INVENTION: POLYMORER: US/10/086,156
CURRENT PILING DATE: 2002-02-28
PRIOR PELLOR DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/274,258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INPORMATION: MAP TO ACO06001.2

OTHER INPORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6

OTHER INPORMATION: EXPRESSED IN PEACH, SIGNAL = 12

OTHER INPORMATION: EXPRESSED IN HEART, SIGNAL = 5.4

OTHER INPORMATION: EXPRESSED IN BEART, SIGNAL = 5.4

OTHER INPORMATION: EXPRESSED IN BEALN, SIGNAL = 7.3

OTHER INPORMATION: EXPRESSED IN BEALN, SIGNAL = 7.3

OTHER INPORMATION: EXPRESSED IN BEALN, SIGNAL = 14

OTHER INPORMATION: EXPRESSED IN HALLOO, SIGNAL = 8.5

OTHER INPORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.5

OTHER INPORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.4

OTHER INPORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 6.4

OTHER INPORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 6.4
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48.3%; Score 305; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.4e-27;
Matches 56; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 69/608,408
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 69/608,408
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 34673
PRIOR PILING DATE: 2001-01-29
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US-UJ-B64-761-346/J

Sequence 34673, Application US/0964761

Sequence 34673, Application US/0964761

GENERAL INPORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hone, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
FRIOR PILING DATE: 2000-02-04
FRIOR PILING DATE: 2000-02-06
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-06-06
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR PILING DATE: 2000-06-06
FRIOR PILING DATE: 2000-06-06
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10024579; Sequence 7, Application US/10024579; Publication No. US20020119522A1; Publication No. US20020119522A1; CENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan; APPLICANT: Gerhardt, Brenda
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1e1 Human Ion Channel-Related Proteins
TITLE OF INVENTION: No. US20020119522A1e1 Human Ion Channel-Related Proteins
TITLE OF INVENTION: No. US20020119522A1e1 Human Ion Channel-Related Proteins
FILE REPRENCE: LEX.-0274-USA
CURRENT FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: US 60/258,595
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENTH: 106
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                                                                                                                                                                                                                        48 BPPEVVPLANGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYV 107
                                                                                                                                             34 QFPEWVPLAIGGAHFTTRLSTLRCYEDTMLASMESGRHYIPTDSEGRYFIDRDGTHFGYV
                                                                                                               1 MVVVTGREPDSRRODGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEPPEVVPLNIGGA
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                                                         2
   DB 14; Length 343;
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Query Match 88.8%; Score 560.5; DB 14; Length Best Local Similarity 91.7%; Pred. No. 1.4e-55; Matches 110; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 SPSTINFVVLAGD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-024-579-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-B64-761-34673
                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-024-579-7
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US-10-086-156-24
Sequence 24, Application US/10086156
Sequence 24, Application No. US20030654989A1
GENERAL INFORMATION:
TUTLE OF INVENTION: POLYNUCLEGITIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: POLYNUCLEGITIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: POLYNUCLEGITIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SU
TITLE OF INVENTION: K+betaM5
FILE REPERENCE: D011SNP
CURRENT APPLICATION NUMBER: US 60/272,190
PRIOR PILING DATE: 2001-02-28
PRIOR PAPLICATION NUMBER: US 60/272,190
PRIOR PLING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENCATION NUMBER: US 60/274,258
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PRI
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PRI
TYPE: PRI
CORGANISM: homo sapiens
US-10-086-156-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDV----LNF-LRSGD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVVVTGREPDSRRQDGAMSSSDAEDDFLEFATPATQAGHALPLLPQRFPEVVPLNIGGA 60
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Pred. No. 1.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                     APPLICANT: SHII, SHIZUKO
APPLICANT: SHIII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAL, KEIICHI
APPLICANT: NAGAL, KEIICHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT PILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SEQ ID NO 2684
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.8%; Score 560.5;
Best Local Similarity 91.7%; Pred. No. 1.1e
Matches 110; Conservative 3; Mismatches
   Sequence 2684, Application US/10094749
Publication No. US20030219741A1
GENDERAL INFORMATION:
                                                                                       APPLICANT: 1SOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: HO, YUKI
APPLICANT: NAGAL, KAORU
APPLICANT: NAGAL, KEIICHI
APPLICANT: IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2684
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Sequence 2684, Ap
Sequence 24, Appl
Sequence 7, Appli
Sequence 39, Appl
Sequence 757, App
Sequence 5, Appli
Sequence 5, Appli
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                                                                                                                                                                                                                                            June 8, 2004, 10:50:19; Search time 959 Seconds (without alignments) 35.204 Million cell updates/sec
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Sequence 4, P
Sequence 7, P
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631
1 MVVVTGREPDSRRQDGAMSS.....GTHFGYVSPSTINFVVLAGD 120
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1: /cgu2_6/ptodata/2/pubpaa/USO7_FUBCOMB.pep:*

2: /cgu2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

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14: /cgu2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

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18: /cgu2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

18: /cgu2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

18: /cgu2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-086-156-24

3 US-10-086-156-24

4 US-10-024-579-7

US-09-864-761-34673

4 US-10-086-156-39

4 US-10-086-156-39

5 US-10-086-156-32

6 US-10-086-156-22

6 US-10-086-156-22

6 US-10-086-156-12

6 US-10-086-156-12

7 US-10-086-156-12

8 US-10-086-156-12

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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        Sequence 25, Appliance 27, Appliance 2
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ALIGNMENTS

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US-10-024-579-5

US-10-024-579-5

US-10-024-579-5

Sequence 5, Application US/10024579

Sequence 5, Application No. US20020119522A1

JEDNICANT: Friddle, Carl Johan

APPLICANT: Friddle, Carl Johan

APPLICANT: Thinger, Exclarate Brenda

APPLICANT: Thinger, C. Alexander Jr.

TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US2002011952A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US2002011952A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US2002011952A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US2002011952A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US2002011952A1el Human Ion Channel-Related Proteins

TITLE OF INVENTION: No. US2002011952A1el Human Ion Channel-Related Proteins

FILE REFERENCE: LEX-0214-USA

CURRENT FILING DATE: 2000-112-18

FROM PROTEIN INVENTION: No. US20020119506

TYPE: PRIOR FILING DATE: 2000-112-8

SEQ ID NO. 5

TYPE: PRIOR

TYPE: PRI
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DB 4; Length 289;

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Query Match
18.8; Score 118.5; DB 4;
Best Local Similarity 36.7%; Pred. No. 1.7e-06;
Matches 33; Conservative 12; Mismatches 38;
FILE REFERENCE: ALBRE-12
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 155
LENGTH: 289
                                                                                                                                                                    TYPE: PRT
CRCANISM: Homo sapiens
US-09-673-395A-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
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Patent No. 6620923

GENERAL INPORMATION:
APPLICANT: SPECHT, THOMAS

APPLICANT: BILNZMAN, BERND
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DALL, BORENTAL, ANDRE
APPLICANT: ROSENTHAL, ANDRE
APPLICANT: ROSENTHAL, ANDRE
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                53 VPLNIGGAHFTFRLSTLRCYEDIMLAAMFSGRHYIPTDSEGRYFIDRDGFHFGYV 107
                                                                                                                                                                                                                                                                                                                                                                                            34 VKLNYGGALYYTTHQTL-TKQDTWLKAMPSGRMEVLTDSEGWILIDRCGRHRGTI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-136-643A-12

Sequence 12, Application US/09336643A

Patent No. 6399761

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Hu, Ping

APPLICANT: Hu, Ping

APPLICANT: Hu, Ping

TITLE OF INVENTION: No. 6399761el Human Potassium Channels

FILE REFERENCE: SEQ-159

CURRENT APPLICATION NUMBER: US/09/336,643A

CURRENT PILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

PRIOR PLING DATE: 1999-01-19

PRIOR PLING DATE: 1999-01-19

PRIOR PLING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PSESEES

SEQ ID NO 12

LENGTH: 258
                                                                                                                                                                                                                                                                     DB 4; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.8%; Score 125; DB 4; Length 258;
Best Local Similarity 40.6%; Pred. No. 2.3e-07;
Matches 26; Conservative 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                                                                                                                  Query Match 21.9%; Score 138.5; DB 4 Best Local Similarity 56.4%; Pred. No. 1.2e-09; Matches 31; Conservative 6; Mismatches 17
     PILE REFERENCE: GENSET.054PR2
CURRENT PEPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5196
LENGTH: 93
                                                                                                                                                                                                ORGANISM: Homo sapiens
US-09-621-976-5196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: H. sapiens
US-09-336-643A-12
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US-09-673-395A-155
                                                                                                                                                                            TYPE: PRT
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82
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                                               2 OPARPGAMAAATAABGVPSRGPPGEVIHLNVGGKRFSTSRQTLTWIPDSFFSSLLSGRI 61
29 EPATPTA-TQAGHALPILIPQEFP--EVVPLNIGGAHFTTRLSTIRCYEDTMLAAMFSGRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 PATPIATOACHALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPT
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Willer, Andrew P.
APPLICANT: Willer, Andrew P.
APPLICANT: Willer, Andrew P.
APPLICANT: Willer, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Warc
TITLE OF INVENTION: No. 6339761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.1%; Score 114; DB 4; Length 25
Best Local Similarity 34.5%; Pred. No. 5.3e-06;
Matches 30; Conservative 16; Mismatches 35; Indels
                                                                                                              86 YIPTDSEGRYFIDRDGTHFGYVSPSTINFV 115
                                                                                                                                                  62 STLKDETGALFIDEDPIVFAPI----LNFL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 DS-EGRYFIDRDGTHFGYVSPSTINFV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 DSLKQHYFIDRDGQMFRYI----LNFL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(256)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-14
                                                                                                                                                                                                                                                                                   US-09-336-643A-14; Sequence 14, Application US/09336643A; Patent No. 6399761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-166-350-12
; Sequence 12, Application US/09166350A
; Patent No. 6440663
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ORGANISM: H. sapiens
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Sequence 25, Appl Sequence 11, Appl Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Ap
                                                                                                                                          June 8, 2004, 10:48:29; Search time 44 Seconds (without alignments) 140.798 Million cell updates/sec
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                                                                                                                                                                                                                                        US-10-024-579-5
631
1 MYVYTGREPDSRRQDGAMSS......GTHFGYVSPSTINFVVLAGD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1ssued Patents AA:*
1: /cgm2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgm2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgm2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgm2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgm2_6/prodata/2/iaa/PcTUS_COMB.pep:*
6: /cgm2_6/prodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-36-643A-12
US-09-36-643A-12
US-09-36-643A-14
US-09-36-643A-14
US-09-36-643A-10
US-09-175-252A-4
US-09-178-109-2
US-09-178-109-2
US-08-606-143-45
US-08-606-143-45
US-08-527-28-1
US-08-527-28-1
US-08-527-12-8
US-08-527-15-2
US-08-527-15-2
US-08-527-15-2
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                                                                                                                                                                                                                                                                                                                                                                                                               389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                Title:
Perfect score:
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No.
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~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		RESULT 1 US-09-336-643A-25 Sequence 25, Applica Patent No. 6399761 GENERAL INFORMATION: APPLICANT: Miler, APPLICANT: Miler, APPLICANT: Waller, APPLICANT: Wang, J TITLE OF INVENTION: FILE REFERENCE: SEQ CURRENT APPLICATION N FILE REFERENCE: SEQ CURRENT APPLICATION N FRIOR PILING DATE: PRIOR PELICATION N PRIOR PILING DATE: TYPE: PRIOR PILING DATE: T	Query Match Best Local Matches 3	දු සි	් සි
0 000000 000000 000 0 0000000 000000 000 0 0 0 0		643A- 25, 100. 63 NIT: PRINT:	Simi 2;	53 VPLN 14 VTLN	113 NFV : 70 NFL
		13A-25 6399761 6399761 FORMATION: FORMATION: FULTAIN MARK Edward FULL PING FRANCE, MARK FRANCE, MARK FRANCE, MARK FRANCE, SEO-15P FRENCE, SEO-15P FRENCE, SEO-15P FRENCE, SEO-178 FRENCE, SEO-	Similarity 50.2; Conservative	VIGGAHFT - : VVGGHLYT	115
100 100 100 100 100 100 100 100 100 100		Andrew P. Andrew P. Mark Edward G. Mark Edward Marc. (1an-Wang No. 639761e P. 159 F. NUSBER: 60/706 1999-03-19 1999-03-19 TOWBER: 60/116 1999-03-18 1999-03-22 1999-02-22 S. 87 S. 87	23.1%; 50.8%; ative	TRLSTL : TSLTTL	
•	Ā	//09336643A P. dward 199761el Hum 19076,687 1-07 60/076,687 60/116,448 1-07 1-07 1-07 1-07 1-07 1-07 1-07 1-07	Sco Pre 7;	RCYBDIM : TRYPDSM	
	ALIGNMENTS	Application US/09336643A Application US/09336643A 299761 1910-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-7 19110-	Score 146; Di Pred. No. 5.1 7; Mismatches	LAAMFSGR LGAMFGGD	
75.5.2 43.6 43.6 43.9 43.19 43.19 43.12 43.13 43.16 43.16 43.16 43.10 43.10 43.10		assium (B 4; e-10; 20;	HYIPTDSI : PPTARDP(
រ៉ា ស៊ី		Shannels	Length 2 Indele	SGRYFIDR 	
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21, Appli 6, Appli 9, Appli 12, Appli 12, Appli 23, Appl 1942, A 1942, Appli 16, Appli 25, Appli 30, Appli 30, Appli 10, Appli 110, Appli 110, Appli 110, Appli 110, Appli 110, Appli 110, Appli			Gaps	3PSTI 112 : :L 69	

RESULT 2
US-09-621-976-5196
Sequence 5196, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.

Sequence 56 AA;

49 PPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104 0; Gaps PPEVVPLNIGGAHFITELSTLRCYEDIMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 56 48.3%; Score 305; DB 5; Length 56; 100.0%; Pred. No. 3e-28; 0; Indels 100.0%; Pred. ... Query Match
Best Local Similarity 100.0
Matches 56; Conservative 쉱

AAM25242 standard; protein; 130 AA.

(first entry) 16-0CT-2001

AAM25242;

Human protein sequence SBQ ID NO:757.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antinfilammatory; antirheumatic; antiarthritic; immunosuppressive; antianfarmatory; antirheumatic; antiarthritic; immunosuppressive; antianfarmatic; antianematic; antianematic; antianematic; antianematic; antianematic; antianematic; antianematic; antidabetic; cycostatic; chematological; antialergic; antialermatic; antidabetic; cycostatic; neuroperotective; antidepressant; nootropic; antidabetic; cycostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianematola arthritis; septic shock; pencreatitis; cardiac dysfunction; neuroperthology; cardiac anaphylaxis; autoimmunity; denetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopennia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; neurological disorder.

Homo sapiens

WO200153455-A2

26-JUL-2001.

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AMM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinitiammacroy; antirteumacit; cristians are expressed in, such as: antinitammacroy; antirteumacit; cristians cardiant; central nervous system; virucide; antiacterial; endocrime; cardiant; cardianteaemic; antiagement; cardiantscatch actiagement; has most partial antiaction; or steopathic; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antiactermatic; nullerary; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidapetic; cytostatic; neuroprotective; antidepressant; nootropic; cristians and polymucleotides are useful for screening for gonding them can be used in gene therapy, antisense therapy and vaccine production, the proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, theumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoictic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, chinitis, asthma, diabetes, cancer, multiple sclerosis, depression, all alsorders expardiaces, neurodegenerative and neurological disease, haematoideservine and neurological disease, parkinson's disease, neurodegenerative and neurological disease.
                                                                                                                                                                                                                                                                                                                                                                           isolated human polynuclectides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 182; 1217pp; English.
22-DEC-2000; 2000WO-US035017.
                                                      23-DEC-1999; 99US-00471275
21-JAN-2000; 2000US-0048B725
25-APR-2000; 2000US-00552317.
                                                                                                                                                                                                                                 Fang YT, Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                     WPI; 2001-457603/49.
N-PSDB; AAH99183.
                                                                                                                                                                       (HYSE-) HYSEQ INC.
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Seguence 130 AA;

1; Gaps 34.9%; Score 220.5; DB 4; Length 130; 78.3%; Pred. No. 9e-18; if Mismatches 11; Indels 1. Ouery Match
Best Local Similarity 78.5.
Then 47; Conservative

ij

1 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHAL-PLLPQEFPEVVPLNIGG 59 82 23 MVVVTGREPDSRRODGAMSSSDAEDDFLEPATPTATOAGHALPPAATGSFLRLFPLTSEG ŝ 셤

completed: June 8, 2004, 10:50:13 Job time : 100 secs Search

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measuring human gene expression in a sample derived from human adult their, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at from wipo.int/pub/published_pct_sequences
         88333333333333333
```

Sequence 56 AA;

ö 49 PPEVVPLNIGGAHFTTRLSTIRCYEDIWLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104 0; Gape 1 PPEKVVPLNIGGAHFTTRLSTLRCYEDTWLAAMPSGRHYIPTDSBGRYFIDRDGTHF 56 48.3%; Score 305; DB 4; Length 56; 100.0%; Pred. No. 3e-28; ive 0; Mismatches 0; Indels Local Similarity 100. 1es 56; Conservative Query Match Best Loc Matches ₹ 셤

AAM02689 standard; protein; 56 AA RESULT 13

AAM02689;

09-OCT-2001 (first entry)

Peptide #1371 encoded by probe for measuring breast gene expression.

Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.

Homo sapiens

WO200157270-A2.

09-AUG-2001

29-JAN-2001; 2001WO-US000661.

2000US-0207456P. 2000US-0060840B. 2000US-00632366. 2000US-0234687P. 2000US-0236359P. 2000US-0180312P 30-JUN-2000; 04-PEB-2000; 26-MAY-2000;

2000GB-00024263 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000; (MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR Hanzel DK, Penn SG,

WPI; 2001-476286/51.

Novel single exon nucleic acid probe used to measuring gene expression in a human breast.

Claim 27; SEQ ID NO 11429; 322pp; English.

The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one auch probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development,

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 mucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes it is now a microarray comprising the novel set of probes acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a

S

Spatially-addressable set of single exon nucleic acid probes, used

Rank DR;

Chen W,

Penn SG, Hanzel DK, WPI; 2002-114183/15 measure gene expression in human lung samples. Claim 27; SEQ ID NO 26427; 634pp; English.

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ö
inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                     Human peptide encoded by genome-derived single exon probe SEQ 1D 26427
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                  49 PPEVVPLANGGAHFITELSTIRCYEDTMIAAMPSGRHYIPTDSEGRYFIDEDGTHF 104
                                                                                                                                         Gape
                                                                                                                                                                                     PPEVVPLAIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
                                                                                                                                                                                                                                                                                                                                                                              Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic Obstructive pulmonary disease; interstital lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; daucher's disease; Niemann-Pick disease;
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                                                                                                             48.3%; Score 305; DB 4; Length 56; 100.0%; Pred. No. 3e-28; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    ABG36762 standard; peptide; 56 AA.
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2000US-0236359P
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                                                                                                                48.38;
                                                                                                                                                                                                                                                                                                                         19-AUG-2002 (first entry)
                                                                                                                                         56; Conservative
                                                                                                                             Local Similarity
                                                                                     Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-2001.
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                                                                                                                                                                                                                                                                                              ABG36762;
                                                                                                                Query Match
                                                                                                                                          Matches
                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                        ABG36762
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
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                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                  49 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe (SENP) (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for gene expression in human adult liver.
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                                                                                                                                                                         Example 4; SEQ ID NO 26807; 650pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                    Score 305; DB 4;
Pred. No. 3e-28;
                                                                                                                                                                                                                                                                                                                                                          48.3%; Sco. 100.0%; Pred. No. ...
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                                                             Rank DR;
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                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0204456P.
30-UJN-2000; 2000US-05604408.
03-AUG-2000; 2000US-00333366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00324289P.
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                                                             Chen W,
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                     56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                             Hanzel DK,
                                                                                             WPI; 2001-483446/52.
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157273-A2
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                                                             Penn SG,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 26807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 PPEVVPLNIGGAHFTTRLSTLRCYEDIMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 27408; 658pp + Sequence Listing; English.
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48.3%; Score 305; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 3e-28;
Matches 56; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         Rank DR
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
                                                                                                                                        04-FBB-2000; 2000US-0180312P.
26-M7X-2000; 2000US-0207456F.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SBP-2000; 2000US-0234687P.
27-SBP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                               30-JAN-2001; 2001WO-US000668
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                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56 AA;
                                               WO200157276-A2
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                    Homo sapiens.
                                                                                09-AUG-2001
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ABB28752 standard; peptide; 56

(first entry)

01-FEB-2002

ABB28752

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ARAL1555). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                              Protein #1374 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 FPEVVPLNIGGAHFTTELSTLRCYBDTALAAMFSGRHYIPTDSEGRYFIDRDGTHF 104
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                                                                                                                                              Human; gene expression; heart; microarray; vascular system;
cardiovascular digease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0204456P.
30-UJX-2000; 2000US-00604408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000666
                                               (first entry)
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                                                                                                                                                                                                congenital heart disease.
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ABB19375;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from Land breast and Er 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acid derived from Exobes with a collection of detectably labelled nucleic acid derived from Exobes with a collection of detectably labelled nucleic acid derived from mean breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the carpeasion of regions of genomic DAA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or proposing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104
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                                                                                                                                                   Peptide #1403 encoded by breast cell single exon nucleic acid probe.
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Claim 27; SEQ ID NO 11720; 327pp + Sequence Listing; English.

comprises number of single exon nucleic acid probes

Rank DR;

Chen W,

Hanzel DK,

Penn SG,

WPI; 2001-496933/54

MOLE-) MOLECULAR DYNAMICS INC

03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P: 27-SEP-2000; 2000US-0236359F. 04-OCT-2000; 2000CB-00024263.

30-JUN-2000; 04-PEB-2000;

26-MAY-2000

30-JAN-2001; 2001WO-US000662

WO200157271-A2 Homo sapiens.

cancer.

09-AUG-2001

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Gaps

48.3%; Score 305; DB 4; Length 56; 100.0%; Pred. No. 3e-28; tive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 56; Conserv Sequence 56 AA;

8 셤 ABB19375 standard; protein; 56 AA

ABB19375 ID ABB1 XX RESULT

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                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP: see AA110068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 PPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Score 305; DB 4; Length 56; 100.0%; Pred. No. 3e-28; ive 0; Mismatches 0; Indels
                                                                                                       Claim 27; SEQ ID NO 19789; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity luv..
Best Local Similarity luv..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157277-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB33939;
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ABB 33939
TO ABB 33939
TO ABB 33939
TO O4-15
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                                                                                                                                                                                                                                                                                                  Peptide #1434 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 PPEVVPLNIGGAHFITRLSTLRCYEDIMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 104
                                                                                  Gaps
                                                                                                             PPRVVPLNIGGAHFITRLSTLRCYEDIMLAAMPSGRHYIPTDSEGRYFIDRDGTHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FPEVVPLNIGGAHFTTRISTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
                                                                                                                            1 PPEVVPLNIGGAHPTITALSTIRCYEDTMIAAMFSGRHYIPIDSBGRYFIDNDGTHF 56
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directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%; Score 305; DB 4; Length 56; 100.0%; Pred. No. 3e-28;
                                                      Length 56;
                                       Score 305; DB 4; Lengta July Pred, No. 3e-28; Dred, No. 3e-28; Indels
                                                                                                                                                                                                                                                                                                                            Probe; microarray; human; placenta; antenatal diagnosis;
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                                               48.3%; Scor.
100.0%; Pred. No. co.
100.0%; Pred. No. co.
100.0%; Pred. No. co.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 27666; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human placenta.
                                                                                                                                                                                                                AAM27397 standard, protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GS-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0380312P.
                                                                                                                                                                                                                                                                        (first entry)
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                                                                                   56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                              genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56 AA;
                            Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      WO200157272-A2
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Best Local S.
Matches 56
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                                                                                                                                                                                                                                           AAM27397;
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                                                         Query Match
                                                                     Local
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Matches
                                                                                                                                                                                       RESULT 7
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RESULT 8 ABB28752

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reperiors in the inventor including a vector sequence encoding the protein. The including a vector sequence encoding the proteins. The nucleic acid and its encoded amino acid sequences are useful in therapeutic, diagnostic and pharmacogenomic applications. The nucleic acid sequences and the encoding pharmacogenomic applications. The nucleic acid sequences and the encoding amino acid sequences are useful in microarrays or other assay formats, to sereen a collection of genetic material from partients that have particular disease, and also in diagnostic or prognostic assays.

CC particular disease, and also in diagnostic or prognostic assays.

CC particular disease, and also in diagnostic or prognostic assays.

CC perceing of drugs effective in the treatment of symptomatic or protein (MHP) in the body. The nucleic acid and the amino acid sequences are useful in diagnosis, drug screening, clinical trial monitoring, the treatment of diseases and disorders and in cosmetic or nutritional creatment of diseases and disorders and in cosmetic or nutritional companient the efficacy of chemotherapeutic agents sequence are necent an envel human membrane protein/ion channel-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 BFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #1397 encoded by probe for measuring cervical gene expression.
                                                                  The invention relates to an isolated nucleic acid molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe, human, microarray, gene expression, cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 385; DB 5; Length 10 Pred, No. 2.5e-37; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
                          Claim 3; Page 12-13; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM14963 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
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03-MG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559F.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.08;
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26-MAY-2000; 2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 SPSTINFVVLAGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 SPSTINFVVLAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matchee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                        New polymucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HFTTRLSTLRCYEDTMLAAMPSGRHYIPTDSBGRYFIDRDGTHFGYVSPSTINFVVLAGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFITELSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDV----LNF-LRSGD 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVVVIGREPDSRRODGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, membrane protein, signal transduction, ion channel; cancer, arthritis; antiviral; cytostatic; antiarthritic; mutritional; cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVVVTGREPDSRRODGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human ion channel-related nucleic acid sequences useful for the treatment of cancer, arthritis or as antiviral agents, in therapeutic, diagnostic and pharmacogenomic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human secretory or membrane proteins (ADA54071. ADA55710) and their coding sequences (ADA52433. ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.8%; Score 560.5; DB 6; Length Best Local Similarity 91.7%; Pred. No. 1.9e-57; Matches 110; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turner CA;
                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 2684; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hilbun E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG70922 standard; protein; 106 AA
(HELI-) HELLY RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel membrane protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2001; 2001US-00024579.
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                                                                , Sugiyama T,
J, Isono Y, H
Yoshikawa T, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerhardt
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(GERH/) GERHARDT B.
(HILB/) HILBUN E.
(TURN/) TURNER C A.
                                                                                                                                                          WPI; 2003-395539/38.
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N-PSDB; ABS55071.
                                                                                                                                                                                  N-PSDB; ADA53477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 289 AA;
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                                                                                          Yamamoto J,
Seki N, Yos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2002
                                                                  Isogai T,
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RESULT ABG7092

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The invention relates to an isolated nucleic acid molecule encoding a novel human membrane protein/ion channel-related protein, including a vector sequence encoding the proteins. The nucleic acid and its encoded amino acid sequences are useful in therapeutic, diagnostic and pharmacogenomic applications. The nucleic acid sequences and the encoding carnino acid sequences are useful in microarrays or other assay formats, to screen a collection of genetic material from patients that have particular medical conditions, and to identify mutations associated with complete acid sequences and the amino acid sequences are useful in screening of drugs effective in the treatment of symptomatic or screening of drugs effective in the treatment of symptomatic or phenotypyth manifestation perturbing the normal function of a new human protein (MHP) in the body. The nucleic acid and the amino acid sequences are useful in diagnosis, drug screening, clinical trial monitoring, the treatment of diseases and diseases and diseases and diseases and diseases and diseases and also according applications. MHPs are useful to treat and in cosmetic or nutritional applications. MHPs are useful to treat and disease or to therapeutically augment the efficacy of chemotherapeutic agents useful in the treatment of cancer, arthritis or as antiviral agents. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of cancer, arthritis or as antiviral agents. The present sequence represents a novel human membrane protein/ion channel-related protein
                                    Claim 3; Page 12; 20pp; English.
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Sequence 120 AA;

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61 HFTTRLSTLRCYBDIWLAAMPSGRHYIPTDSBGRYFIDRDGTHPGYVSPSTINFVVLAGD 120
                                                                                                                                                                                   61 HFTTRLSTLRCYEDTWLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTINFVVLAGD 120
                                                                                9
                                                                                                                 1 MVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA 60
                                                                           1 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA
                                        Gaps
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    Length 120;
                                        0; Indels
  100.0%; Score 631; DB 5;
100.0%; Pred. No. 2.7e-66;
                                        0; Mismatches
Query Match
Best Local Similarity 100.
Matches 120; Conservative
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AAB15537 standard; protein; 271 AA AAB15537;

(first entry) 28-FEB-2001

Human immune system molecule from Incyte clone 2751129.

antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic; cancer; antigout; dermatological; antithyroid; viruside; hepatotropic; antibody; immunosuppressive; cytostatic; fungicide; protozocacide; antibacterial; gene therapy; diagnostic; immunological disorder; viral infection; bacterial infection; fungal infection; parasitic infection; immunogen. Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic; RESCULT 2
AAB15537
ID AAB1
XX
AX
AX
DT 28-P
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DT 28-P
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AALI
KW KW AALI
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KW WPI
KW WDI
KW WPI

Homo sapiens

WO200060080-A2

12-OCT-2000.

04-APR-2000; 2000WO-US009072

99US-0127852P. 05-APR-1999; 05-MAY-1999;

(INCY-) INCYTE PHARM INC.

Lu DAM; Baughn MR, Azimzai Y, Tang YT, Yue H, Lal P,

WPI; 2000-665005/64. N-PSDB; AAA95776.

New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial infections

Claim 1; Page 77; 95pp; English

This sequence represents a human immune system molecule (IMOL) encoded by the cDMA isolated as Clone 2771129 from the Incyte THPIAZSOB library. The human IMOLS (AABEISSO) and their encoding polymucleotides (AAASS775-A55789), and compositions comprising them are useful for the diagnosis, treatment or prevention of immunological disorders, infections and cell proliferative disorders associated with decreased expression or activity of IMOL, such as immunological disorders (e.g. inflammation, activity of IMOL, such as immunological disorders (e.g. inflammation, activity of IMOL, such as immunological disorders (e.g. inflammation, cotinit keratosis, hastomyces), parasites (e.g. inflammation, hapergillus, Blastomyces), parasites (e.g. parvovirus, coronavirus), coronavirus), coronavirus, arteriosclerosis, bursatis), and cancers (e.g. actinic keratosis, arteriosclerosis, bursitis), and cancers (e.g. actinic corona). The peptides are also useful as immunogens for the polynucleotides may be used to detect and quantify gene expression in decent and quantify gene expression in disease, as targets in a microarray, to detect differences in gene sequences among normal, carrier and affected individuals, and for screening libraries of compounds in drug screening techniques. Antibodies which specifically bind to IMOL may be used for the diagnosis of minibitors of the patients being treated with IMOL or agonists, or inhibitors of IMOL

Sequence 271 AA;

ä 61 HFTTRLSTLRCYEDTWLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTINFVVLAGD 120 9 1 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATFATQAGHALPLLPQEFPEVVPLNIGGA 61 HPTTRLSTLRCYBDIMLAAMPSGRHYIPTDSBGRYFIDRDGTHFGDV----LNF-LRSGD 1 MVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA 5; Gaps Length 271; 2; Indels DB 3; Score 560.5; DB 3 Pred. No. 1.7e-57; 3; Mismatches 2 88.8%; Matches 110; Conservative Query Match Best Local Similarity ð 쉽 ₽

RESULT 3

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ADAS5116 Btandard; protein; 289 AA ADA55116;

Human protein, SEQ ID 2684.

(first entry)

20-NOV-2003

Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.

Homo sapiens.

EP1293569-A2

19-MAR-2003

21-MAR-2002; 2002BP-00006586.

14-SEP-2001; 2001JP-00328381. 24-JAN-2002; 2002US-0350435P.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compagen Ltd.
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OM protein - protein search, using sw model

June Run on:

8, 2004, 09:37:55 ; Search time 96 Seconds (without alignments) 353.184 Million cell updates/sec

US-10-024-579-5 631 1 MVVVTGREPDSRRQDGAMSS.....GTHFGYVSPSTINFVVLAGD 120 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 8eq Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* Database

geneseqp2003as: *
geneseqp2003bs: *
geneseqp2004s: * geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* geneseqp1990s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abg70921 Human nov	Aab15537 Human imm	Ada55116 Human pro	Abg70922 Human nov		Abb33939 Peptide #		N	Abb19375 Protein #	Aam67102 Human bon	Aam54702 Human bra	Abg48768 Human liv	Aam02689 Peptide #		Human	Aag03290 Human sec	Adc31345 Human nov		Abb60184 Drosophil		Aam25877 Human pro	Aay34129 Human pot	Aam93682 Human pol	Human	Aab95201 Human pro
SUMMAKIBS	ID	ABG70921	AAB15537	ADA55116	ABG70922	AAM1 4963	ABB33939	AAM27397	ABB28752	ABB19375	AAM67102	AAM54702	ABG48768	AAM02689	ABG36762	AAM25242	AAG03290	ADC31345	AAE32081	ABB60184	ABJ10887	AAM25877	AAY34129	AAM93682	AAU27754	AAB95201
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	Length	120	271	289	106	56	56	26	26		99	56	56	26	26	130	, 76	455	473	228	228	272	237	237	237	237
de	Query	100.0	88.8	88.8	61.0	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	34.9	34.1	25.9	25.9	23.9	23.9	23.3	23.1	23.1	23.1	23.3
	Score	631	560.5	560.5	385	305	305	305	305	305	305	305	305	305	305	220.5	215	163.5	163.5	150.5	150.5	147	146	146	146	146
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ABP53973	ABJ10891	ABJ10892	ABP51811	ABP51311	ABP69573	AAE10329	ABB65078	ABP53981	ABJ10904	AAE28631	AAM93832	ABG60220	ABU11829	AAM39908	ABG72171	AB014767	ABP58347 .	AAG13411	AAG13410	
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237	237	237	237	252	290	339	301	301	301	301	237	150	225	329	329	329	329	289	298	
23.1	23.1	23.1	23.1	23.1	23.1	23.1	22.5	22.5	22.5	22.5	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.0	22.0	
146	146	146	146	146	146	146	142	142	142	142	141	140.5	140.5	140.5	140.5	140.5	140.5	139	139	
56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

ABG70921 standard; protein; 120 AA. Human novel membrane protein #2. (first entry) 10-DEC-2002 ABG70921; RESULT 1 741X88X1X88X1X111111111111X8X8X8X8X8X8X1X8

Human; membrane protein; signal transduction; ion channel; SNP; cancer; arthritis; antiviral; cytostatic; antiarthritic; nutritional; cosmetic; single nucleotide polymorphism.

Homo sapiens.

/note= "May be Arg or Ser as a result of a single nucleotide polymorphism" Location/Qualifiers Key Misc-difference

/note= "May be Pro or leu as a result of a single nucleotide polymorphism" Misc-difference

Misc-difference

/note= "May be Ala or Ser as a result of a single nucleotide polymorphism"

US2002119522-A1

29-AUG-2002

18-DEC-2001; 2001US-00024579

28-DEC-2000; 2000US-0258595P.

FRIDDLE C J. GERHARDT B. HILBUN E. TURNER C A. FRID/)

(GERH/) (HILB/) (TURN/)

Turner CA; Hilbun E, 'n Friddle CJ, Gerhardt

WPI; 2002-731353/79. N-PSDB; ABS55072.

New human ion channel-related nucleic acid sequences useful for the treatment of cancer, arthritis or as antiviral agents, in therapeutic, diagnostic and pharmacogenomic applications.

Location/Qualifiers

FEATURES

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/organism="Bomo sapiens"
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(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Standt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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AMCNUC:NRDG1-00092-D9-A nrdg1 (10855) Rattus norvegicus cDNA clone
Drdg1-00092-d9 5', mRNA sequence.
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317 CACTTCACTACACGCCTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCATG 396
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Bukaryota; Mezacas Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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DNA Sequencing by: M.B. Soares Lab
Clone distribution: WC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www.bio.llnl.gov/bbrp/image/fimage.html
The following repetitive elements were found in this cDNA
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Plate: 00092 row: d column: 9.
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68.9%; Score 250; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.3e-45;
Matches 250; Conservative 0; Mismatches 0;
                                                                                                   sequence:
99-137, >GC_rich#Low_complexity
Seq primer: M13 Forward
                                                                                                                                                       Location/Qualifiers
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
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                            /mol_type="mRNA"
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/nove="Voctor: pSPORT1; Site_1: Sall; Site_2: Not1; rat dorsal root ganglia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TACTCTGCGGCGCTATGAAGACACCATGCTGGCGCCATGTTCAGCGGGGGGGCATTACAT
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                                                                                                                                                                                                                       Length 620;
                                                                                                                                                                                                                   tch 68.5%; Score 248.8; DB 14; Length al Similarity 89.3%; Pred. No. 2.8e-45; Conservative 0; Mismatches 32; Indels
             /organism="Rattus norvegicus"
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Job time: 2530 secs
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Homo sapiens
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                                                                                                                                  160 ATGCTGGTAGTGACGGGGGGGGGCCAGACGCCGTCACTCGGACGGTGCCATGTCCAGC 219
                                                                                                                                                                                     220 TCCGAAGCCGAAGACGACTTCCTGGAGCCGGCCACTCCTACGGCCACGCAAGGCGGGGCAC 279
                                                                                                                                                                                                                                                                                                       280 GGGCTGCCCCTGCTGCCCCAGAGTTTCCTGAAGTCGTCCCCTTGAACATTGGAGGGGGCT 339
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, M., Hiranoto, K., Hiraoka, T., Hiraoka, T., Inotani, K., Inotani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Saraki, T., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, P., Sato, K., Shinata, T., Tomaru, A., Toyar, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizahi, Y., Watahiki, A., Yasunishi, A., Rikku Encyclopedia of Mouse Pull-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIXEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIXEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome_ree@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
grepare full-length cDNA libraries for rapid discovery of new
genes. Genome Ree. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matshuki,K., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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71.8%; Score 260.8; DB 10; Length 652; 88.4%; Pred. No. 6e-48; Ative 0; Mismatches 37; Indels 0;
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                                                  Matches 283; Conservative
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UI-HF-ENO-afs-e-10-0-UI.rl NIH MGC_50 Homo sapiens cDNA clone IMAGE:3067867 5', mRNA sequence.
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugabara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Flease visit our web site (http://genome.gsc.riken.go.jp) for further details.
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1 (basea I to 460.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emali: cgapbs-rémail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procureant: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol type="manA"
/mol type="manA"
/strain="CSTBL/65"
/db_xref="taxon:10090"
/clone="g370042112"
/clone=lib="RIKEN full-length enriched, B16 F10Y cells"
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603073846F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5165722 5',
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1 (Dases 1 to 978)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arraye by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMILI row: 1 column: 11
High quality sequence stop: 730.
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                                                         organism="Homo sapiens"
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/mol_type="mRNA"
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/lab_host="DH10B"
/clone=lib="MTH MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vectory is oligo-df primed and directionally cloned (EccNv site is destroyed upon cloning). Average insert size 1.3 kb, insert size and directionally cloned (EccNv site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0716 row: E column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.2%; Score 294.8; DB 12; Length 978; llarity 98.8%; Pred. No. 1.8e-55; Conservative 0; Mismatches 2; Indels 2;
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BU902852 AGENCOURT
B1827921 603073846
CF162776 B0716E09-
BY722445 BY722445
                                                                                                                                                                 June 8, 2004, 09:16:07; Search time 2522 Seconds (without alignments) 4298.165 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                            1 atggtggtagtcacggggcg......tagtcctagcaggtgattag 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55026578
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BI827921
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Gapop 10.0 , Gapext 1.0
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Query
Match Length DB
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Perfect score:
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62.4 72.3 6551 10 BB 62.4 72.3 655 10 BB 62.4 72.3 658 10 BB 62.4 72.3 3269 111 AK 60.8 72.3 3269 111 AK 60.8 71.9 652 10 BB 72.0 68.5 68.5 68.5 69.6 11 BB 72.2 68.5 69.6 11 BB 72.2 68.5 69.6 11 BB 72.2 69.	66666666666666666666666666666666666666	54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54090 54	125 bp 171 House, Crass; Cat 1. gov/. 1. h.b Ma 1. ph.b 1. life? 1. Life? 1. Life? 2. Column 1. Crass; Cat
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US-10-086-156-29

| Sequence 29, Application US/10086156 |
| Sequence 29, Application US/10086156 |
| Sequence 29, Application World US20030054989A1 |
| GENERAL INFORMATION: |
| APPLICANT: Bristol-Myers Squibb Company |
| TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SI |
| TITLE OF INVENTION: |
| TITLE OF INVENTION: |
| TITLE OF INVENTION: |
| FILE REFERENCE: D0115NP |
| CURRENT APPLICANTION NUMBER: US 60/272,190 |
| PRIOR PILING DATE: 2001-02-28 |
| PRIOR PLING DATE: 2001-02-28 |
| PRIOR PILING DATE: 2001-03-07 |
| NUMBER OF SEQ ID NOS: 98 |
| SEQ ID NOS: 98 |
| SEQ ID NO 29 |
| LENGTH: 583 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 TGGAGCCGGCCACGCCGACGGCCACGCCGGGGCACGCGCTGCCCCTGCTGCCGACAGG 142
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CTHER INFORMATION: MAP TO ACOGGOD: 2

COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN HERRY, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HET414, SIGNAL = 8.5

OTHER INFORMATION: EXPRESSED IN HUG, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4

US-09-864-761-1385
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Best Local Similarity 86.8%; Pred. No. 8.1e-62)
Matches 244; Conservative 0; Mismatches 3?
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US-10-086-156-29
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hansel, David R.
TITLE OF INVERTION: GENE EXPRESSION ANALYSIS BY MICROARDAY
ITLE REPRESENCE: Accordica-X-1.
CURRENT APPLICATION WADRE: UG/09/864, 75,
CURRENT PALLING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-23
FRIOR PRING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-23
FRIOR PRING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-23
FRIOR PLI
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                                                                                                                                                                                                                                                                                              CACTICACTACACGCCTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATG 525
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GCCACACATTTGGGTATGT 320
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ORGANISM: Homo sapiens
PEATURE:
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US-09-864-761-1385/C
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APPLICANT: OTSUIXA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: TRIE, KYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEXI, NACHIKA, TSUTOMU
APPLICANT: OTSUIXA, MCTOTOKI
APPLICANT: OTSUIXA, MCTOTOKI
APPLICANT: OTSUIXA, MCTOTOKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
FILE REFERENCE: 084335/0160
CURRENT FILING DATE: 2002-03-12
FRIOR FILING DATE: 2002-03-12
FRIOR APPLICATION NUMBER: 5P 2001-328381
FRIOR FILING DATE: 2001-09-14
NUMBER: OF SEQ ID NOS: 3381
SEQ ID NO 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1045, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGCACACACTTTGGGTATGT 320
SOFTWARE: pt_Fl_genes Version 2.0
SEQ ID NO 408
LENGTH: 1068
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APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUNO
APPLICANT: ISONO, YUNO
APPLICANT: HO, YUKI
                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LACATION: (100)...(1068)
; US-10-120-988-408
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Sequence 23, Application US/10086156

Publication No. US20030054989A1

SEQUENCE 23, Application US/10086156

Publication No. US20030054989A1

SEQUENCE 23, Application No. US2003005498A1

SEQUENCE 24, APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: EDITORIES ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUITITLE OF INVENTION: EDITORIES: US/10/086,156

CURRENT APPLICATION NUMBER: US/10/086,156

CURRENT PLING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/272,190

PRIOR APPLICATION NUMBER: US 60/274,258

PRIOR APPLICATION NUMBER: US 60/274,258

PRIOR PLING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 98

SOFTWARE PATENTLY VERSION 3.0
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288 CACTTCACTACACGCCTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATG
                                                                                                                                                                                                                                                                                                                                                228 GCGCTGCCCCTGCTGCCACAGGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGCT
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                                                                                                           DB 16; Length 2576;
                                                                                                                                                              2; Indels
                                                                                                           Score 316.8; DB 1
Pred. No. 1.6e-92;
                                                                                                                                                              0; Mismatches
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                                                                                                           87.3%;
                                                                                                        Query Match
Best Local Similarity 99.44
Matches 318; Conservative
TYPE: DNA
CORGANISM: Homo sapiens
US-10-094-749-1045
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ORGANISM: homo sapiens
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; LOCATION: (1)..(1029)
US-10-086-156-23
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Sequence 18, Application US/10296115
Sequence 18, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 7046CT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT PILING DATE: 2002-11-18
FRIOR PILING DATE: 2000-01-21
FRIOR PLING DATE: 2000-01-21
FRIOR PLING DATE: 2000-01-21
FRIOR PLING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-21
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-21
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Best Local Similarity 99.4%; Pred. No. 1.1e-92;
Matches 318; Conservative 0; Mismatches 2; Indels 0;
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Sequence 408, Application US/10120988

Publication No. US20030219745A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Ton

APPLICANT: Goodrich, Ryle

APPLICANT: Mang, Dunrui

APPLICANT: Nen, Felyan

APPLICANT: Wang, Dunrui

CURRENT APPLICATION NUMBER: US/10/120,988

CURRENT APPLICATION NUMBER: 09/174,528

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441
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; ORGANISM: Homo sapiens
US-10-296-115-18
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558 TAG 560
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                                                                                                                                                                                                                                                                                                         TTCAGTGGGGCGCACTACATCCCCCACGACTCCGAGGCCGGTACTTCATCGACCGGAT 300
CACTTCACTACACGCCTGTCCACACTGCGGTGCTACGAAGACACCCATGTTGGCAGCCATG 240
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                                                                                                                                                                                                                                                                      TTCAGTGGGCGCCACTACATCCCCACGGACTCCGAGGGCCGGFACTTCATCGACCGAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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100.0%; Score 363; DB 14; Length 680;
Best Local Similarity 100.0%; Pred. No. 1.2e-107;
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US-10-024-579-8
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TAG 363
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Sequence 9850, Ap Sequence 9851, Ap Sequence 2266, A Sequence 653, App Sequence 11, App Sequence 106, App Sequence 10, App Sequence 10, App Sequence 1285, App Sequence 1285, App Sequence 1285, App Sequence 21, App Sequence 22, App Sequence 23, App Sequence 24, App Sequence 23, App Sequence 24, App Sequence 22, App Sequence 1058, Ap Sequence 1058, App Sequence 11, App Sequenc

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Sequence 8, Appli
Sequence 18, Appli
Sequence 408, Appl
Sequence 1045, Appl
Sequence 23, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 30, Appl
                                                                                                                          8, 2004, 09:30:35 ; Search time 348 Seconds (without alignments) 4758.634 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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14 US-10-024-579-8

13 US-10-026-115-18

16 US-10-086-1408

16 US-10-086-156-23

19 US-09-864-761-1385

15 US-10-026-156-29

15 US-09-864-761-1385

15 US-09-864-761-18144

15 US-09-864-761-18144

16 US-09-910-943-1391

10 US-09-910-943-1391

10 US-09-910-943-1391

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10 US-09-910-9849
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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363
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No.
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ALIGNMENTS

RESULT 1

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APPLICANT: Fiddle. Carl Johan
APPLICANT: Fiddle. Carl Johan
APPLICANT: Fiddle. Carl Johan
APPLICANT: Fiddle. Series
APPLICANT: Torner. Carlact. Breade
APPLICANT: Turner. C. Alexander Jr.
APPLICANT: Turner. C. Alexander Jr.
TITLE OF INVENTION: and Polymucleotides Encoding the Same
TITLE OF INVENTION: and Polymucleotides Encoding the Same
TITLE OF INVENTION: and Polymucleotides Encoding the Same
CURRENT APPLICANTON NUMBER: US 10/024,579
CURRENT APPLICANTON NUMBER: US 60/258,595
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GCGCTGCCCTGCTGCCACAGGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGCT 180
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Sequence 4, Application US/10024579 Publication No. US20020119522A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              : homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local S
Matches 363
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM:
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            60 L1 AND (ION CHANNEL#)
=> duplicate remove
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DUPLICATE PREFERENCE IS 'USPATFULL, PCTFULL'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L2
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L3
=> d 1-60
     ANSWER 1 OF 60 USPATFULL on STN
L_3
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AN
       Human proteins having transmembrane domains and cDNAs encoding these
TT
       proteins
TN
       Kato, Seishi, Sagamihara-shi, JAPAN
       Sekine, Shingo, Ageo-shi, JAPAN
       Sagami Chemical Research Center, Sagamihara-shi, JAPAN (non-U.S.
PA
       corporation)
       Protegene, Inc., Tokyo, JAPAN (non-U.S. corporation)
PI
       US 2004048339
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                               20040311
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AΙ
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       Continuation of Ser. No. US 2000-529100, filed on 21 Aug 2000, ABANDONED
RLI
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       UNKNOWN
PRAI
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DT
       Utility
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FS
LN.CNT 2285
INCL
       INCLM: 435/069.100
       INCLS: 435/320.100; 435/325.000; 530/350.000; 536/023.500
NCL
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1.3
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AN
ΤT
       Human proteins having hyprophobic domains and dnas encoding these
       proteins
       Kato, Seishi, Sagamihara-shi, JAPAN
TN
       Kimura, Tomoko, Tsuchiura-shi, JAPAN
PΤ
       US 2004034192
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              536/023.500; 435/320.100; 435/325.000; 435/069.100; 530/388.100
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L3
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AN
       Novel human proteins, polynucleotides
TT
       encoding them and methods of using the same
       Gangolli, Esha A., Madison, CT, UNITED STATES
IN
       Spytek, Kimberly A., New Haven, CT, UNITED STATES
       Gilbert, Jennifer, Madison, CT, UNITED STATES
       Casman, Stacie, North Haven, CT, UNITED STATES
       Blalock, Angela, Branford, CT, UNITED STATES
       Li, Li, Branford, CT, UNITED STATES
       Vernet, Corine, Branford, CT, UNITED STATES
       Shenoy, Suresh, Branford, CT, UNITED STATES
       Mishra, Vishnu S., Gainesville, FL, UNITED STATES
       Furtak, Katarzyna, Ansonia, CT, UNITED STATES
       Gerlach, Valerie L., Branford, CT, UNITED STATES
       Edinger, Shlomit, New Haven, CT, UNITED STATES
       Malyanker, Uriel, Branford, CT, UNITED STATES
       Stone, David, Guilford, CT, UNITED STATES
       Millet, Isabelle, Milford, CT, UNITED STATES
       Smithson, Glennda, Guilford, CT, UNITED STATES
       Gunther, Erik, Branford, CT, UNITED STATES
       Ellerman, Karen, Branford, CT, UNITED STATES
       Padigaru, Muralidhara, Branford, CT, UNITED STATES
       Taupier, Raymond J., JR., East Haven, CT, UNITED STATES
       Anderson, David W., Branford, CT, UNITED STATES
PΙ
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
       Novel Human proteins, polynucleotides
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       encoding them and methods of using the same
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Zerhusen, Bryan D., Branford, CT, UNITED STATES

IN

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Kekuda, Ramesh, Norwalk, CT, UNITED STATES
       Spytek, Kimberly A., New Haven, CT, UNITED STATES
       Shenoy, Suresh G., Branford, CT, UNITED STATES
       Miller, Charles E., Guilford, CT, UNITED STATES
       Hjalt, Tord, Lomma, SWEDEN
       Gerlach, Valerie, Branford, CT, UNITED STATES
       Baumgartner, Jason C., New Haven, CT, UNITED STATES
       Guo, Xiaojia (Sasha), Branford, CT, UNITED STATES
       Gangolli, Esha A., Madison, CT, UNITED STATES
       Vernet, Corine A. M., Branford, CT, UNITED STATES
       Padigaru, Muralidhara, Branford, CT, UNITED STATES
       Li, Li, Branford, CT, UNITED STATES
       Pena, Carol E. A., New Haven, CT, UNITED STATES
       Gorman, Linda, Branford, CT, UNITED STATES
       Anderson, David W., Branford, CT, UNITED STATES
       Edinger, Schlomit R., New Haven, CT, UNITED STATES
       Patturajan, Meera, Branford, CT, UNITED STATES
       Stone, David J., Guilford, CT, UNITED STATES
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
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       Novel human proteins, polynucleotides
TI
       encoding them and methods of using the same
       Li, Li, Branford, CT, UNITED STATES
IN
       Furtak, Katarzyna, Ansonia, CT, UNITED STATES
       Perna, Amanda, Hamden, CT, UNITED STATES
       Patturajan, Meera, Branford, CT, UNITED STATES
       Shimkets, Richard A., Guilford, CT, UNITED STATES
       Guo, Xiaojia Sasha, Branford, CT, UNITED STATES
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Burgess, Catherine E., Wethersfield, CT, UNITED STATES
       Malyankar, Uriel M., Branford, CT, UNITED STATES
       Tchernev, Velizar T., Branford, CT, UNITED STATES
       Vernet, Corine A., Branford, CT, UNITED STATES
       Spytek, Kimberly A., New Haven, CT, UNITED STATES
       Agee, Michele, Wallingford, CT, UNITED STATES
       Rastelli, Luca, Guilford, CT, UNITED STATES
       Shenoy, Suresh G., Branford, CT, UNITED STATES
       Grosse, William M., Branford, CT, UNITED STATES
       Alsobrook, John P., II, Madison, CT, UNITED STATES
       Lepley, Denise M., Branford, CT, UNITED STATES
       Gerlach, Valerie, Branford, CT, UNITED STATES
       Edinger, Schlomit R., New Haven, CT, UNITED STATES
       MacDougall, John R., Hamden, CT, UNITED STATES
       Peyman, John A., New Haven, CT, UNITED STATES
       Gunther, Erik, Branford, CT, UNITED STATES
       Stone, David J., Guilford, CT, UNITED STATES
       Ellerman, Karen, Branford, CT, UNITED STATES
       Gangolli, Esha A., Madison, CT, UNITED STATES
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
       2003:301031 USPATFULL
ΤI
       Novel human proteins, polynucleotides
       encoding them and methods of using the same
       Spytek, Kimberly A., New Haven, CT, UNITED STATES
IN
       Li, Li, Branford, CT, UNITED STATES
       Edinger, Shlomit R., New Haven, CT, UNITED STATES
       Ellerman, Karen, Branford, CT, UNITED STATES
       Stone, David J., Guilford, CT, UNITED STATES
       Malyankar, Uriel M., Branford, CT, UNITED STATES
       Shimkets, Richard A., Guilford, CT, UNITED STATES
       Guo, Xiaojia Sasha, Branford, CT, UNITED STATES
       Anderson, David W., Branford, CT, UNITED STATES
       Patturajan, Meera, Branford, CT, UNITED STATES
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Casman, Stacie J., North Haven, CT, UNITED STATES

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Gerlach, Valerie, Branford, CT, UNITED STATES
       Gusev, Vladimir Y., Madison, CT, UNITED STATES
       Kekuda, Ramesh, Norwalk, CT, UNITED STATES
       Gorman, Linda, Branford, CT, UNITED STATES
       Zerhusen, Bryan D., Branford, CT, UNITED STATES
       Baumgartner, Jason C., New Haven, CT, UNITED STATES
       Tchernev, Velizar T., Branford, CT, UNITED STATES
       Vernet, Corine A.M., Branford, CT, UNITED STATES
       Smithson, Glennda, Guilford, CT, UNITED STATES
Shenoy, Suresh G., Branford, CT, UNITED STATES
       Liu, Xiaohong, Lexington, MA, UNITED STATES
       MacDoughall, John R., Hamden, CT, UNITED STATES
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
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ΤI
       HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS ENCODING THESE
       PROTEINS
       KATO, SEISHI, KANAGAWA, JAPAN
IN
       SEKINE, SHINGO, SAITAMA, JAPAN
       KIMURA, TOMOKO, KANAGAWA, JAPAN
       KOBAYASHI, MIDORI, KANAGAWA, JAPAN
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       US 2003092175 A1
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Berghs, Constance, New Haven, CT, UNITED STATES

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ΑN
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       Human NIM1 kinase
       Bandman, Olga, Mountain View, CA, UNITED STATES
IN
       Molteni, Angela, Cantu, ITALY
       Magnaghi, Paola, UNITED STATES
       Bosotti, Roberta, Nerviano, ITALY
       Scacheri, Emanuela, UNITED STATES
       Isacchi, Antonella, UNITED STATES
       Hodgson, David M., Ann Arbor, MI, UNITED STATES
       Incyte Genomics, Inc., Palo Alto, CA (U.S. corporation)
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       Signal peptide-containing proteins
TI
       Lal, Preeti G., Santa Clara, CA, UNITED STATES
TN
       Au-Young, Janice, Brisbane, CA, UNITED STATES
       Reddy, Roopa, Sunnyvale, CA, UNITED STATES
       Murry, Lynn E., Fayetteville, AR, UNITED STATES
       Mathur, Preete, Fremont, CA, UNITED STATES
PΙ
       US 2003073162
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AΤ
       Continuation-in-part of Ser. No. US 1999-271110, filed on 17 Mar 1999,
RLI
       ABANDONED Continuation-in-part of Ser. No. US 1997-966316, filed on 7
       Nov 1997, GRANTED, Pat. No. US 5932445
DT
       Utility
       APPLICATION
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              435/070.300; 435/183.000; 435/320.100; 435/325.000; 435/326.000;
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
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       Novel human ion channel proteins and polynucleotides
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encoding the same
       Walke, D. Wade, Spring, TX, UNITED STATES
IN
       Mathur, Brian, The Woodlands, TX, UNITED STATES
       Turner, C. Alexander, JR., The Woodlands, TX, UNITED STATES
       Friddle, Carl Johan, The Woodlands, TX, UNITED STATES
       Gerhardt, Brenda, Spring, TX, UNITED STATES
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
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ΤI
       Novel human proteins, polynucleotides
       encoding them and methods of using the same
IN
       Taupier, Raymond J., JR., New Haven, CT, UNITED STATES
       Padigaru, Muralidhara, Branford, CT, UNITED STATES
       Spytek, Kimberly A., New Haven, CT, UNITED STATES
       Burgess, Catherine E., Wethersfield, CT, UNITED STATES
       Vernet, Corine A.M., North Branford, CT, UNITED STATES
       Fernandes, Elma R., Branford, CT, UNITED STATES
       Shimkets, Richard A., West Haven, CT, UNITED STATES
       Liu, Xiaohong, Branford, CT, UNITED STATES
       Majumder, Kumud, Stamford, CT, UNITED STATES
       Colman, Steven D., Guilford, CT, UNITED STATES
       Zerhusen, Bryan D., Branford, CT, UNITED STATES
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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TI
       Isolated human kinase proteins, nucleic acid molecules encoding human
```

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kinase proteins, and uses thereof
       Yan, Chunhua, Boyd, MD, UNITED STATES
IN
       Ketchum, Karen A., Germantown, MD, UNITED STATES
       Di Francesco, Valentina, Rockville, MD, UNITED STATES
       Beasley, Ellen M., Darnestown, MD, UNITED STATES
       APPLERA CORPORATION, Norwalk, CT, UNITED STATES, 06856-5435 (U.S.
PA
       corporation)
       US 2003022229
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       NCLS: 530/350.000; 435/006.000; 435/252.300; 435/320.100; 435/325.000
IC
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       ICM: C120001-68
       ICS: C07H021-04; C12N009-12; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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       2002:337390 USPATFULL
AN
TI
       Human polynucleotides, polypeptides, and antibodies
       Moore, Paul A., Germantown, MD, UNITED STATES
IN
       Coleman, Timothy A., Gaithersburg, MD, UNITED STATES
       Gentz, Reiner L., Rockville, MD, UNITED STATES
       Dillon, Patrick J., Carlsbad, CA, UNITED STATES
       Ni, Jian, Germantown, MD, UNITED STATES
       Li, Yi, Sunnyvale, CA, UNITED STATES
       Endress, Gregory A., Florence, MA, UNITED STATES
       Soppet, Daniel R., Centreville, VA, UNITED STATES
PΙ
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FS
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       ICM: C12P021-02
       ICS: C12N005-06; C07H021-04; C12N009-00; C07K014-435
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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L3
ΑN
       2002:287612 USPATFULL
       Novel human ion channel protein and polynucleotides
ΤI
       encoding the same
IN
       Friddle, Carl Johan, The Woodlands, TX, UNITED STATES
       Hilbun, Erin, Houston, TX, UNITED STATES
       Turner, C. Alexander, JR., The Woodlands, TX, UNITED STATES
PΙ
       US 2002160475
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ΑI
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DT
       Utility
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APPLICATION
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       ICS: C12N009-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L3
     ANSWER 15 OF 60 USPATFULL on STN
       2002:272888 USPATFULL
AN
       Human polynucleotides, polypeptides, and antibodies
TΙ
       Ni, Jian, Germantown, MD, UNITED STATES
IN
       Shi, Yanggu, Gaithersburg, MD, UNITED STATES
       Ebner, Reinhard, Gaithersburg, MD, UNITED STATES
       Ruben, Steven M., Olney, MD, UNITED STATES
       Human Genome Sciences, Inc., Rockville, MD, UNITED STATES, 20850 (U.S.
PA
       corporation)
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       ICS: C12Q001-68; C07H021-04; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
ΤI
       Isolated human transporter proteins, nucleic acid molecules encoding
       human transporter proteins, and uses thereof
TN
       Merkulov, Gennady, Baltimore, MD, UNITED STATES
       Guegler, Karl, Menlo Park, CA, UNITED STATES
       Brandon, Rhonda C., Laytonsville, MD, UNITED STATES
       Di Francesco, Valentina, Rockville, MD, UNITED STATES
       Beasley, Ellen M., Darnestown, MD, UNITED STATES
PI
       US 2002142376
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AΙ
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RLI
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DТ
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LN.CNT 3248
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TC
       ICM: C12P021-02
       ICS: C12N005-06; C07K014-435; C07H021-04; C12N009-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
```

ANSWER 17 OF 60 USPATFULL on STN

L3

```
AN
       2002:228449 USPATFULL
ΤI
       Novel human proteins, polynucleotides
       encoding them and methods of using the same
       Gerlach, Valerie L., Branford, CT, UNITED STATES
IN
       Ellerman, Karen, Branford, CT, UNITED STATES
       MacDougall, John R., Hamden, CT, UNITED STATES
       Smithson, Glennda, Guilford, CT, UNITED STATES
PΙ
                                20020905
       US 2002123612
                           A1
       US 2001-898570
                                20010703 (9)
ΑI
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PRAI
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       US 2000-210809P
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       ICS: C07H021-04; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 18 OF 60 USPATFULL on STN
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AN
       2002:221403 USPATFULL
ΤI
       ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
       KINASE PROTEINS, AND USES THEREOF
IN
       Yan, Chunhua, Boyds, MD, UNITED STATES
       Ketchum, Karen A., Germantown, MD, UNITED STATES
       Di Francesco, Valentina, Rockville, MD, UNITED STATES
       Beasley, Ellen M., Darnestown, MD, UNITED STATES
PI
       US 2002119544
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                                20020829
       US 6492154
                          B2
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TC
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 19 OF 60 USPATFULL on STN
L3
ΑN
       2002:221399 USPATFULL
TI
       Novel human ion channel protein and polynucleotides
       encoding the same
IN
       Friddle, Carl Johan, The Woodlands, TX, UNITED STATES
       Hilbun, Erin, Houston, TX, UNITED STATES
       Gerhardt, Brenda, Spring, TX, UNITED STATES
       Turner, C. Alexander, JR., The Woodlands, TX, UNITED STATES
```

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DT
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       ICS: C12N009-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 20 OF 60 USPATFULL on STN
L3
       2002:221382 USPATFULL
AN
       Novel human ion channel-related proteins and
TI
       polynucleotides encoding the same
       Friddle, Carl Johan, The Woodlands, TX, UNITED STATES
TN
       Gerhardt, Brenda, Spring, TX, UNITED STATES
       Hilbun, Erin, Houston, TX, UNITED STATES
       Turner, C. Alexander, JR., The Woodlands, TX, UNITED STATES
                      A1 20020829
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       US 2002119522
       US 2001-24579
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PRAI
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TC
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       ICM: C12P021-02
       ICS: C12N005-06; C07H021-04; C07K014-435
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L3
     ANSWER 21 OF 60 USPATFULL on STN
AN
       2002:206777 USPATFULL
TI
       Novel human ion channel protein and polynucleotides
       encoding the same
IN
       Yu, Xuanchuan Sean, Houston, TX, UNITED STATES
       Miranda, Maricar, Houston, TX, UNITED STATES
                     A1
PΙ
       US 2002111478
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       US 2001-34843
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L3
     ANSWER 22 OF 60 USPATFULL on STN
AN
       2002:148637 USPATFULL
TI
       Novel human ion channel proteins and polynucleotides
       encoding the same
IN
       Turner, C. Alexander, JR., The Woodlands, TX, UNITED STATES
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Mathur, Daniel, Wooster, OH, UNITED STATES
       Mathur, Brian, The Woodlands, TX, UNITED STATES
PΙ
       US 2002076780
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       INCLM: 435/183.000
       INCLS: 530/350.000; 536/023.200
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       NCLS: 530/350.000; 536/023.200
TC
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       ICS: C07H021-04
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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AN
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       Human Sec6 vesicle transport protein
IN
       Labrie, Samuel T., St. Peters, MO, UNITED STATES
       Streeter, David G., Boulder Creek, CA, UNITED STATES
ΡI
       US 2002055108
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                               20020509
ΑI
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                               20010613 (9)
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       Sep 1997, GRANTED, Pat. No. US 5989818
DT
       Utility
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       NCLS: 435/183.000; 435/069.100; 435/325.000; 435/320.100; 536/023.200
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L3
    ANSWER 24 OF 60 USPATFULL on STN
ΑN
       2002:78847 USPATFULL
TI
       Novel human ion channel protein and polynucleotides
       encoding the same
       Hu, Yi, The Woodlands, TX, UNITED STATES
IN
       Kieke, James Alvin, Houston, TX, UNITED STATES
       Turner, C. Alexander, JR., The Woodlands, TX, UNITED STATES
       Nehls, Michael C., Stockdorf, GERMANY, FEDERAL REPUBLIC OF
       Friedrich, Glenn, Houston, TX, UNITED STATES
       Zambrowicz, Brian, The Woodlands, TX, UNITED STATES
       Sands, Arthur T., The Woodlands, TX, UNITED STATES
       US 2002042505
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       US 2001-825147
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IC
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       ICS: C12N009-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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ANSWER 25 OF 60 USPATFULL on STN
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       2002:346980 USPATFULL
AN
       cDNAs coding for human proteins having transmembrane domains
ΤI
       Kato, Seishi, Sagamihara, JAPAN
IN
       Sekine, Shingo, Ageo, JAPAN
       Sagami Chemical Research Center, Kanagawa, JAPAN (non-U.S. corporation)
PA
       Protogene, Inc., Tokyo, JAPAN (non-U.S. corporation)
       US 6500939
                               20021231
PΙ
                          B1
       WO 9918199 19990415
                               20000821 (9)
       US 2000-529157
AΙ
       WO 1998-JP4447
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DT
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EXF
       435/325; 435/320.1; 435/366; 435/23.1; 536/23.1
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L3
       ANSWER 26 OF 60
                       PCTFULL
                                   COPYRIGHT 2004 Univentio on STN
AN
       2002098900 PCTFULL ED 20021218 EW 200250
TIEN
       NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES
       ENCODING THEM AND METHODS OF USING THE SAME
       NOUVELLES PROTEINES HUMAINES, POLYNUCLEOTIDES LES CODANT ET METHODES
TIFR
       D'UTILISATION ASSOCIEES
       ZERHUSEN, Bryan, D., 337 Monticello Drive, Branford, CT 06405, US [US,
IN
       KEKUDA, Ramesh, 71 Aiken Street, Unit R3, Norwalk, CT 06851, US [IN,
       SPYTEK, Kimberly, A., 28 Court Street, Number 1, New Haven, CT 06511, US
       [US, US];
       SHENOY, Suresh, G., 15 Millwood Drive, Branford, CT 06405, US [IN, US];
       MILLER, Charles, E., 98 Saddle Hill Drive, Guilford, CT 06437, US [US,
       HJALT, Tord, 514 Main Street, Apartment 30, East Haven, CT 06512, US
       [SE, US];
       GERLACH, Valerie, L., 18 Rock Pasture Road, Branford, CT 06405, US (US,
       BAUMGARTNER, Jason, C., 1697 Quinnipiac Avenue, New Haven, CT 06513, US
       [US, US];
       GUO, Xiaojia, 713 Robert Frost Drive, Branford, CT 06405, US [CN, US];
       GANGOLLI, Esha, A., 31 Strawberry Hill Road, Madison, CT 06443, US [IN,
       US];
       VERNET, Corine, A., M., Apartment L6, 1739 Foxon Road, Branford, CT
       06471, US [FR, US];
       PADIGARU, Muralidhara, 71 Hampton Park, Branford, CT 06405, US [IN, US];
       LI, Li, 56 Jerimoth Drive, Branford, CT 06405, US [CN, US];
       PENA, Carol, E., A., 604 Orange Street, Number 2, New Haven, CT 06511.
       US [US, US];
       GORMAN, Linda, 329 Monticello Drive, Branford, CT 06405, US [US, US];
       ANDERSON, David, W., 85 Montoya Drive, Branford, CT 06405, US [US, US];
       EDINGER, Shlomit, R., 766 Edgewood Avenue, New Haven, CT 06515, US [US,
      US];
       PATTURAJAN, Meera, Apartment 1C, 45 Harrison Avenue, Branford, CT 06405,
      US [IN, US];
       STONE, David, J., 223 Whitehorn Drive, Guilford, CT 06437, US [US, US]
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PA
       06511, US [US, US], for all designates States except US;
       ZERHUSEN, Bryan, D., 337 Monticello Drive, Branford, CT 06405, US [US,
       US], for US only;
       KEKUDA, Ramesh, 71 Aiken Street, Unit R3, Norwalk, CT 06851, US [IN,
       US], for US only;
       SPYTEK, Kimberly, A., 28 Court Street, Number 1, New Haven, CT 06511, US
       [US, US], for US only;
       SHENOY, Suresh, G., 15 Millwood Drive, Branford, CT 06405, US [IN, US],
       for US only;
       MILLER, Charles, E., 98 Saddle Hill Drive, Guilford, CT 06437, US [US,
       US], for US only;
       HJALT, Tord, 514 Main Street, Apartment 30, East Haven, CT 06512, US
       [SE, US], for US only;
       GERLACH, Valerie, L., 18 Rock Pasture Road, Branford, CT 06405, US [US,
       US], for US only;
       BAUMGARTNER, Jason, C., 1697 Quinnipiac Avenue, New Haven, CT 06513, US
       [US, US], for US only;
       GUO, Xiaojia, 713 Robert Frost Drive, Branford, CT 06405, US [CN, US],
       for US only;
       GANGOLLI, Esha, A., 31 Strawberry Hill Road, Madison, CT 06443, US [IN,
       US], for US only;
       VERNET, Corine, A., M., Apartment L6, 1739 Foxon Road, Branford, CT
       06471, US [FR, US], for US only;
       PADIGARU, Muralidhara, 71 Hampton Park, Branford, CT 06405, US [IN, US],
       for US only;
       LI, Li, 56 Jerimoth Drive, Branford, CT 06405, US [CN, US], for US only;
       PENA, Carol, E., A., 604 Orange Street, Number 2, New Haven, CT 06511,
       US [US, US], for US only;
       GORMAN, Linda, 329 Monticello Drive, Branford, CT 06405, US [US, US],
       for US only;
       ANDERSON, David, W., 85 Montoya Drive, Branford, CT 06405, US [US, US],
       for US only;
       EDINGER, Shlomit, R., 766 Edgewood Avenue, New Haven, CT 06515, US [US.
       US], for US only;
       PATTURAJAN, Meera, Apartment 1C, 45 Harrison Avenue, Branford, CT 06405,
       US [IN, US], for US only;
       STONE, David, J., 223 Whitehorn Drive, Guilford, CT 06437, US [US, US],
       for US only
ΑG
       ELRIFI, Ivor, R., Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.,
       C., One Financial Center, Boston, MA 02111, US
LAF
       English
LA
       English
DT
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_{
m PI}
       WO 2002098900
                            A2 20021212
DS
       W:
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US 2001-60/299,230
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US 2002-10/161,927
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ANSWER 27 OF 60
                 PCTFULL
                            COPYRIGHT 2004 Univentio on STN
2002081629 PCTFULL ED 20021028 EW 200242
NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES
ENCODING THEM AND METHODS OF USING THE SAME
NOUVELLES PROTEINES HUMAINES, POLYNUCLEOTIDES CODANT CELLES-CI ET
PROCEDE D'UTILISATION DE CEUX-CI
SPYTEK, Kimberly, A., 28 Court Street, Number 1, New Haven, CT 06511, US
[US, US];
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EDINGER, Shlomit, R., 766 Edgewood Avenue, New Haven, CT 06515, US [US,
ELLERMAN, Karen, 87 Montoya Drive, Branford, CT 06405, US [US, US];
STONE, David, J., 223 Whitethorn Drive, Guilford, CT 06437, US [US, US];
MALYANKAR, Uriel, M., 229 Branford Road, Number 330, Branford, CT 06405,
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[US, US];
GUO, Xiaojia, 713 Robert Frost Drive, Branford, CT 06405, US [CN, US];
ANDERSON, David, W., 85 Montoya Drive, Branford, CT 06405, US [US, US];
PATTURAJAN, Meera, 45 Harrison Avenue, Apartment 1C, Branford, CT 06405,
US [IN, US];
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GERLACH, Valerie, 18 Rock Pasture Road, Branford, CT 06405, US [US, US];
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06512, US [US, US];
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BURGESS, Catherine, E., 90 Carriage Hill Drive, Wethersfield, CT 06109,
US [US, US];
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GUSEV, Vladimir, Y., 1209 Durham Road, Madison, CT 06443, US [UA, US];
KEKUDA, Ramesh, 1213 Avalon Valley Drive, Danbury, CT 06810, US [IN,
GORMAN, Linda, 392 Monticello Drive, Branford, CT 06405, US [US, US];
ZERHUSEN, Bryan, D., 337 Monticello Drive, Branford, CT 06405, US [US,
BAUMGARTNER, Jason, C., 1697 Quinnipiac Avenue, New Haven, CT 06513, US
[US, US];
TCHERNEV, Velizar, T., 45 Jefferson Road #3-12, Branford, CT 06405, US
[BG, US];
VERNET, Corine, A., M., 1739 Foxon Road, Apartment L6, Branford, CT
06471, US [FR, US];
SMITHSON, Glennda, 125 Michael Drive, Guildford, CT 06435, US [US, US];
HEYES, Melvyn, P., 183 Townsend Avenue, Number 3, New Haven, CT 06512,
US [GB, US];
SHENOY, Suresh, G., 15 Millwood Drive, Branford, CT 06405, US [IN, US];
LIU, Xiaohong, 96 Montoya Circle, Branford, CT 06405, US [US, US];
GANGOLLI, Esha, A., 31 Strawberry Hill Road, Madison, CT 06443, US [IN,
```

L3

ΑN

TIEN

TIFR

IN

CURAGEN CORPORATION, 555 Long Wharf Drive, 11th Floor, New Haven, CT PA 06511, US [US, US], for all designates States except US; SPYTEK, Kimberly, A., 28 Court Street, Number 1, New Haven, CT 06511, US [US, US], for US only; LI, Li, 56 Jerimoth Road, Branford, CT 06405, US [CN, US], for US only; EDINGER, Shlomit, R., 766 Edgewood Avenue, New Haven, CT 06515, US [US, US], for US only; ELLERMAN, Karen, 87 Montoya Drive, Branford, CT 06405, US [US, US], for US only; STONE, David, J., 223 Whitethorn Drive, Guilford, CT 06437, US [US, US], for US only; MALYANKAR, Uriel, M., 229 Branford Road, Number 330, Branford, CT 06405, US [IN, US], for US only; SHIMKETS, Richard, A., 5 Indian Meadows Drive, Guilford, CT 06437, US [US, US], for US only; GUO, Xiaojia, 713 Robert Frost Drive, Branford, CT 06405, US [CN, US], for US only; ANDERSON, David, W., 85 Montoya Drive, Branford, CT 06405, US [US, US], for US only; PATTURAJAN, Meera, 45 Harrison Avenue, Apartment 1C, Branford, CT 06405, US [IN, US], for US only; BERGHS, Constance, 459 Orange Street, New Haven, CT 06511, US [NL, US], for US only; GERLACH, Valerie, 18 Rock Pasture Road, Branford, CT 06405, US [US, US], for US only; TAUPIER, Raymond, J., Jr., 34 Pardee Place Extension, East Haven, CT 06512, US [US, US], for US only; PENA, Carol, E., A., 604 Orange Street, Number 2, New Haven, CT 06511, US [US, US], for US only; PADIGARU, Muralidhara, 71 Hampton Park, Branford, CT 06405, US [IN, US], for US only; LIU, Yi, 470 Prospect Street, Number 53, New Haven, CT 06511, US [CN, US], for US only; BURGESS, Catherine, E., 90 Carriage Hill Drive, Wethersfield, CT 06109, US [US, US], for US only; MILLER, Charles, E., 98 Saddle Hill Drive, Guilford, CT 06437, US [US, US], for US only; GUSEV, Vladimir, Y., 1209 Durham Road, Madison, CT 06443, US [UA, US], for US only; KEKUDA, Ramesh, 1213 Avalon Valley Drive, Danbury, CT 06810, US [IN, US], for US only; GORMAN, Linda, 392 Monticello Drive, Branford, CT 06405, US [US, US], for US only; ZERHUSEN, Bryan, D., 337 Monticello Drive, Branford, CT 06405, US [US. US], for US only; BAUMGARTNER, Jason, C., 1697 Quinnipiac Avenue, New Haven, CT 06513, US [US, US], for US only; TCHERNEV, Velizar, T., 45 Jefferson Road #3-12, Branford, CT 06405, US [BG, US], for US only; VERNET, Corine, A., M., 1739 Foxon Road, Apartment L6, Branford, CT 06471, US [FR, US], for US only; SMITHSON, Glennda, 125 Michael Drive, Guildford, CT 06435, US [US, US], for US only; HEYES, Melvyn, P., 183 Townsend Avenue, Number 3, New Haven, CT 06512, US [GB, US], for US only; SHENOY, Suresh, G., 15 Millwood Drive, Branford, CT 06405, US [IN, US], for US only; LIU, Xiaohong, 96 Montoya Circle, Branford, CT 06405, US [US, US], for US only; GANGOLLI, Esha, A., 31 Strawberry Hill Road, Madison, CT 06443, US [IN, US], for US only AG ELRIFI, Ivor, R., Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, One Financial Center, Boston, MA 02111, US

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LAF
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       LAL, Preeti, G., P.O. Box 5142, Santa Clara, CA 95056, US [IN, US]
       INCYTE GENOMICS, INC., 3160 Porter Drive, Palo Alto, CA 94304, US [US,
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       STREETER, David, G., Incyte Genomics, Inc., 3160 Porter Drive, Palo
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       CODANT DES PROTEINES TRANSPORTEURS HUMAINES, ET UTILISATIONS ASSOCIEES
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       PE CORPORATION (NY), 761 Main Avenue, Norwalk, CT 06859, US [US, US]
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TIFR
       CODANT POUR CES PROTEINES
IN
       FRIDDLE, Carl, Johan, 127 S. Goldenvine Circle, The Woodlands, TX 77382,
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TIFR
       PROTEINES KINASES HUMAINES ISOLEES, MOLECULE D'ACIDE NUCLEIQUE CODANT
       CES PROTEINES KINASES HUMAINES ET LEURS UTILISATIONS
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       NOUVELLE PROTEINE HUMAINE DE CANAUX IONIOUES ET POLYPEPTIDES LA CODANT
       YU, Xuanchuan, 7900 N. Stadium #101, Houston, TX 77030, US;
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       ISHIMOTO, Lance, K., LEXICON GENETICS INCORPORATED, 4000 Research Forest
       Drive, The Woodlands, TX 77381, US
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\mathbf{AN}
       NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES
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       PROTEINES HUMAINES, POLYNUCLEOTIDES LES CODANT ET PROCEDES D'UTILISATION
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      MALYANKAR, Uriel, 229 Brandford Road #330, Branford, CT 06405, US [IN,
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       TAUPIER, Raymond, J., Jr., 34 Pardee Place Extension, East Haven, CT
       06512, US [US, US], for US only;
       ANDERSON, David, 43A Linden Avenue, Brandord, CT 06405, US [US, US], for
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       ELRIFI, Ivor, R., Mintz, Levin, Cohn, Ferris, Glovsky & Popeo, P.C .,
AG
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       FRIDDLE, Carl, Johan, 127 S. Goldenvine Circle, The Woodlands, TX 77382,
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TIFR
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[FR, US], for US only;
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US [US, US], for US only;
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ELLERMAN, Karen, 87 Montoya Drive, Branford, CT 06405, US [US, US], for
US only;
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for US only
ELRIFI, Ivor, R., Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C.,
One Financial Center, Boston, MA 02111, US
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       FRIDDLE, Carl, Johan, 127 S. Goldenvine Circle, The Woodlands, TX 77382,
IN
       HILBUN, Erin, 16222 Stuebner Airline, Spring, TX 77379, US;
       GERHARDT, Brenda, 2123 Knollbrook Lane, Spring, TX 77373, US;
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       LEXICON GENETICS INCORPORATED, 4000 Research Forest Drive, The
PΑ
       Woodlands, TX 77381, US [US, US]
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TURNER, C., Alexander, Jr., 67 Winter Wheat Place, The Woodlands, TX
IN
       77381, US;
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       LEXICON GENETICS INCORPORATED, 4000 Research Forest Drive, The
PA
       Woodlands, TX 77381, US [US, US]
       ISHIMOTO, Lance, K., Lexicon Genetics Incorporated, 4000 Research Forest
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AN
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TIEN
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TIFR
       NOUVELLES PROTEINES DU CANAL IONIQUE HUMAIN ET POLYNUCLEOTIDES CODANT
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       WALKE, D., Wade;
IN
       MATHUR, Brian;
       TURNER, C., Alexander, Jr.;
       FRIDDLE, Carl, Johan;
       GERHARDT, Brenda
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       IDENTIFICATION AND ISOLATION OF NOVEL POLYPEPTIDES HAVING PDZ DOMAINS
TIEN
       AND METHODS OF USING SAME
       IDENTIFICATION ET ISOLEMENT DE NOUVEAUX POLYPEPTIDES COMPORTANT DES
TIFR
       DOMAINES PDZ ET LEURS METHODES D'UTILISATION
IN
       HERRERO, Juan;
       PIROZZI, Gregorio;
       UVEGES, Albert
       AXCELL BIOSCIENCES CORPORATION
PA
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       ENCODING THEM AND METHODS OF USING THE SAME
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       PERMETTANT DE LES UTILISER
       TAUPIER, Raymond, J., Jr.;
IN
       VERNET, Corine, A., M.;
       FERNANDES, Elma;
       SHIMKETS, Richard, A.;
       MAJUMDER, Kumud;
       PADIGARU, Muralidhara;
       COLMAN, Steven, D.;
       ZERHUSEN, Bryan, D.;
       SPYTEK, Kimberly, A.;
       BURGESS, Catherine, E.;
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       VERNET, Corine, A., M.;
       FERNANDES, Elma;
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       PADIGARU, Muralidhara;
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       HU, Yi;
IN
       KIEKE, James, Alvin;
       TURNER, Alexander, C., Jr.;
       NEHLS, Michael, C.;
       FRIEDRICH, Glenn;
       ZAMBROWICZ, Brian;
       SANDS, Arthur, T.
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AN
       HUMAN POLYNUCLEOTIDES, POLYPEPTIDES, AND ANTIBODIES
TIEN
TIFR
       POLYNUCLEOTIDES, POLYPEPTIDES ET ANTICORPS HUMAINS
IN
       MOORE, Paul, A.;
       NI, Jian;
       SOPPET, Daniel, R.;
       COLEMAN, Timothy, A.;
       GENTZ, Reiner, L.;
       ENDRESS, Gregory, A.;
       LI, Yi;
       DILLON, Patrick, J.
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       MOORE, Paul, A.;
       NI, Jian;
       SOPPET, Daniel, R.;
       COLEMAN, Timothy, A.;
       GENTZ, Reiner, L.;
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AN
       HUMAN POLYNUCLEOTIDES, POLYPEPTIDES, AND ANTIBODIES
TIEN
       POLYNUCLEOTIDES, POLYPEPTIDES ET ANTICORPS HUMAINS
TIFR
IN
       NI, Jian;
       SHI, Yanggu;
       EBNER, Reinhard;
       CHOI, Gil, H.;
       RUBEN, Steven, M.
       HUMAN GENOME SCIENCES, INC.;
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       NI, Jian;
       SHI, Yanggu;
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       HUMAN POLYNUCLEOTIDES, POLYPEPTIDES, AND ANTIBODIES
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       POLYNUCLEOTIDES, POLYPEPTIDES ET ANTICORPS HUMAINS
IN
       RUBEN, Steven, M.;
       SHI, Yanggu
       HUMAN GENOME SCIENCES, INC.;
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TIEN
       HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE
       PROTEINS
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       PROTEINES HUMAINES A DOMAINES HYDROPHOBES ET ADN CODANT CES PROTEINES
IN
       KATO, Seishi;
       KIMURA, Tomoko
       PROTEGENE INC.;
PA
       SAGAMI CHEMICAL RESEARCH CENTER;
       KATO, Seishi;
       KIMURA, Tomoko
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       PROTEINES HUMAINES A DOMAINES HYDROPHOBES ET ADN CODANT POUR CES
TIFR
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       KATO, Seishi;
IN
       KIMURA, Tomoko
PΑ
       SAGAMI CHEMICAL RESEARCH CENTER;
       PROTEGENE INC.;
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       PROTEINES
       KATO, Seishi;
TN
       KIMURA, Tomoko
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SAGAMI CHEMICAL RESEARCH CENTER;
PA
       PROTEGENE INC.;
       KATO, Seishi;
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       KATO, Seishi;
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       ROSEN, Craig, A.;
IN
       RUBEN, Steven, M.;
       KOMATSOULIS, George
PΑ
       HUMAN GENOME SCIENCES, INC.;
       ROSEN, Craig, A.;
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       KOMATSOULIS, George
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       KATO, Seishi;
IN
       KIMURA, Tomoko
PA
       SAGAMI CHEMICAL RESEARCH CENTER;
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IN
       KATO, Seishi;
       KIMURA, Tomoko
PA
       SAGAMI CHEMICAL RESEARCH CENTER;
       PROTEGENE INC.;
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       KATO, Seishi;
IN
       KIMURA, Tomoko
       SAGAMI CHEMICAL RESEARCH CENTER;
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       PROTEGENE INC.;
       KATO, Seishi;
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       KATO, Seishi;
IN
       KIMURA, Tomoko
PΑ
       SAGAMI CHEMICAL RESEARCH CENTER;
       PROTEGENE INC.;
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IN
       KATO, Seishi;
       SEKINE, Shingo;
       KIMURA, Tomoko;
      NAKAMURA, Nobuko
PΑ
       SAGAMI CHEMICAL RESEARCH CENTER;
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       KATO, Seishi;
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       SAGAMI CHEMICAL RESEARCH CENTER;
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       KATO, Seishi;
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PA
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